

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 133.491 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-1

Perfect score: 120

Sequence: 1 QVQLVQSGAEVKFGASVKVCKAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1980s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	25	8	Adq90697 Anti-VEGF
2	120	100.0	25	8	Adq07258 IL-9 anti
3	120	100.0	25	8	Adt88325 Human IL-
4	120	100.0	25	8	Adu80305 Heavy cha
5	120	100.0	25	9	Ady31444 Human ant
6	120	100.0	25	9	Ady31447 Human ant
7	120	100.0	25	9	Ady31453 Human ant
8	120	100.0	25	9	Ady31459 Human ant
9	120	100.0	25	9	Ady31468 Human ant
10	120	100.0	30	2	Aar27045 Human hea
11	120	100.0	30	2	Aaw79211 Framework
12	120	100.0	30	5	Aae19676 Human gro
13	120	100.0	30	5	Aau70462 Human hea
14	120	100.0	30	9	Adw87138 Anti-huma
15	120	100.0	30	9	Adx01239 Humanized
16	120	100.0	30	9	Adx27022 Human gro
17	120	100.0	30	9	Ady31315 Human ant
18	120	100.0	30	9	Ady31321 Human ant
19	120	100.0	30	9	Ady31327 Human ant
20	120	100.0	30	9	Ady31332 Human ant
21	120	100.0	30	9	Ady31336 Human ant
22	120	100.0	30	9	Ady59169 Anti-Tag-
23	120	100.0	30	9	Aeb13671 Human ant
24	120	100.0	32	6	Abr61972 Monoclonal

25	120	100.0	32	6	ABR57347	ABR57347 MatDC16 V
26	120	100.0	37	8	ABO55410	ABO55410 Human gen
27	120	100.0	54	8	ABO59987	ABO59987 Human gen
28	120	100.0	58	9	ABO20856	ABO20856 Human var
29	120	100.0	69	7	ADK18820	ADK18820 Anti-huma
30	120	100.0	71	6	ABJ18728	ABJ18728 VH antibo
31	120	100.0	71	6	ABJ18731	ABJ18731 VH antibo
32	120	100.0	71	6	ABJ18730	ABJ18730 VH antibo
33	120	100.0	71	6	ABJ18729	ABJ18729 Human sub
34	120	100.0	80	7	ABG75309	ABG75309 Human sub
35	120	100.0	80	8	ABM79521	ABM79521 Human DP7
36	120	100.0	87	2	AAR2991	AAR2991 Homologou
37	120	100.0	92	5	ABG78172	ABG78172 Human Fv
38	120	100.0	92	5	ABG91863	ABG91863 Human ant
39	120	100.0	96	7	ADC99825	ADC99825 Anti-huma
40	120	100.0	96	7	ADD05429	ADD05429 Anti-MUC1
41	120	100.0	96	7	ADF09867	ADF09867 Anti-MUC1
42	120	100.0	97	2	AAR57475	AAR57475 Human HV3
43	120	100.0	97	2	AAR92078	AAR92078 Human HV3
44	120	100.0	97	5	ABG31425	ABG31425 Amino aci
45	120	100.0	98	3	AAV50952	AAV50952 Human ant

ALIGNMENTS

RESULT 1

ADQ90697

ID ADQ90697 standard; peptide; 25 AA.

XX AC ADQ90697;

XX AC ADQ90697;

DT 21-OCT-2004 (first entry)

XX DE Anti-VEGF antibody heavy chain FR1 subgroup I peptide SEQ ID NO:1.

XX KW antibody; antigen binding fragment; cell culture; variable domain;

XX KW modified framework region; hypervariable region; cytotstatic;

KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;

KW tumour; inflammatory disorder; angiogenic disorder;

KW immunological disorder; anti-VEGF antibody;

KW anti vascular endothelial cell growth factor antibody; heavy chain; FR1.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO2004065417-A2.

XX PD 05-AUG-2004.

XX XX 23-JAN-2004; 2004WO-US001844.

XX PR 23-JAN-2003; 2003US-0442484P.

XX PA (GETH) GENENTECH INC.

XX PI Simmons Lr;

XX XX WPI; 2004-562149/54.

DR Producing an antibody or antigen binding fragment in high yield in a cell

XX culture, comprises expressing a variable domain with a modified framework

PT region in a host cell.

XX Claim 15; SEQ ID NO 1; 161pp; English.

XX The present invention describes a method for producing an antibody or

CC antigen binding fragment in high yield in a cell culture. The method

CC comprises expressing a variable domain of the antibody or antigen binding

CC fragment comprising a modified framework region (FR) in a host cell, and

CC recovering the antibody or antigen binding fragment variable domain

CC comprising the modified framework from the host cell. The modified FR in

CC the method described above has a substitution of at least one amino acid

CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents a heavy chain FRI peptide of an anti-VSGF (vascular
 CC endothelial cell growth factor) antibody, which is used in the
 CC exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 120; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
 |||||
 Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 2

ADU07258

ID ADU07258 standard; peptide; 25 AA.

AC ADU07258;

DT 13-JAN-2005 (first entry)

DE IL-9 antibody variable heavy chain (VH) framework region 1 sequence #1.

XX Respiratory infection; human; interleukin-9 antagonist; IL-9;
 KW respiratory syncytial virus; anti-RSV antigen antibody;
 KW leukotriene modifier; asthma-like symptom; wheezing; allergy;
 KW immunomodulatory; anti-inflammatory; anti-viral; antibiotic; antifungal;
 KW mast cell modulator; virucide; antibacterial; fungicide; antiasthmatic;
 KW antiallergic; IL-9 antibody; variable heavy chain; VH; framework region.

XX Homo sapiens.

XX WO2004091519-A2.

XX 28-OCT-2004.

XX 12-APR-2004; 2004WO-US011329.

XX 11-APR-2003; 2003US-0462307P.

PR 10-JUN-2003; 2003US-0477801P.

XX (MEDI-) MEDIMMUNE INC.

XX Reed JL;

XX WPI; 2004-775524/76.

XX Managing, treating or ameliorating in a human subject a respiratory
 PT infection or its symptoms caused by bacteria, fungi or respiratory
 PT syncytial virus by administering an IL-9 antagonist.

XX Disclosure; SEQ ID NO 33; 276pp; English.

XX The invention relates to a method of managing, treating or ameliorating a
 CC respiratory infection or its symptom in a human subject by administering

CC an interleukin-9 (IL-9) antagonist. The method further comprises
 CC administering to the subject an anti-respiratory syncytial virus (anti-
 CC RSV) antigen antibody. The anti-RSV antigen antibody is palivizumab. The
 CC method further comprises administering a leukotriene modifier, which is
 CC montelukast, zafirlukast, pranlukast or zileuton. Also disclosed are: a
 CC method of preventing the development, onset or progression of asthma or
 CC one or more asthma-like symptoms in a child, a method of preventing,
 CC managing, treating or ameliorating wheezing in a pre-term infant, infant
 CC or child, a method of preventing, managing, treating or ameliorating
 CC wheezing in a human subject, and a method of preventing, managing,
 CC treating or ameliorating asthma or an allergy or its symptoms in a human
 CC subject. Preventing the development, onset or progression of asthma or
 CC one or more asthma-like symptoms in a child having or previously having a
 CC respiratory infection comprises administering an IL-9 antagonist.
 CC Preventing, managing, treating or ameliorating wheezing in a pre-term
 CC infant, infant or child comprises administering an IL-9 antagonist. The
 CC method further comprises administering at least one other therapy that is
 CC not administration of an IL-9 antagonist. Preventing, managing, treating
 CC or ameliorating wheezing in a human subject comprises administering an IL
 CC -9 antagonist and at least one other therapy that is not administration
 CC of an IL-9 antagonist. The therapy is an immunomodulatory agent, an anti-
 CC inflammatory agent, an anti-viral agent, an antibiotic, an antifungal
 CC agent or a mast cell modulator. The method further comprises
 CC administering to the subject a leukotriene modifier, an anti-histamine,
 CC an anti-immunoglobulin E (IgE) antibody, an anti-IL-4 antibody or a mast
 CC cell protease inhibitor. Preventing, managing, treating or ameliorating
 CC asthma or an allergy or its symptoms in a human subject comprises
 CC administering an IL-9 antagonist and at least one other asthma or allergy
 CC therapy. The IL-9 antagonist is an antibody that immunospecifically binds
 CC to an IL-9 receptor (IL-9R) or its subunit or to an IL-9 polypeptide. The
 CC methods are useful in managing, treating or ameliorating in a human
 CC subject a respiratory infection or its symptoms caused by bacteria, fungi
 CC or RSV. This sequence represents a framework region from an antibody
 CC against IL-9.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 120; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
 |||||
 Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 3

ADT88325

ID ADT88325 standard; peptide; 25 AA.

XX AC ADT88325;

XX 13-JAN-2005 (first entry)

XX Human IL-19 antibody VH framework region 1 seqid 33.

XX respiratory; antiinflammatory; immunosuppressive; antiasthmatic;
 KW antiallergic; antiarthritic; neuroprotective; antirheumatic; immunotoxin;
 KW angiogenesis inhibitor; TNF alpha antagonist; IL-9 antagonist; IL-9;
 KW IL-9 antibody; 4D4; 4D4 H2-1 D11; 4D4com-XF9; 4D4com-2F9; 7F3; 71A10;
 KW 22D3; 7F3com-2H2; 7F3com-3H5; 7F3com-3D4; IL-9 associated disorder;
 KW respiratory infection; respiratory syncytial virus; parainfluenza virus;
 KW human metapneumovirus; inflammatory disorder; asthma; allergy; arthritis;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW framework region 1; variable heavy chain.

XX Homo sapiens.

XX WO2004091510-A2.

XX 28-OCT-2004.

XX 12-APR-2004; 2004WO-US011172.

XX 11-APR-2003; 2003US-0462259P.
PR 10-JUN-2003; 2003US-0477737P.
XX (MEDI-) MEDIMMUNE INC.
XX Reed JL;
XX WPI; 2004-775520/76.
XX New IL-9 antibody comprising a variable heavy or light domain or a
PT complementarity determining region having an amino acid sequence of e.g.,
PT 4D4, useful in treating or preventing e.g., respiratory infection or
PT inflammatory disorder.
XX Disclosure; SEQ ID NO 33; 291pp; English.
XX The invention describes a new IL-9 antibody comprising: a variable heavy
CC (VH) or variable light (VL) domain having an amino acid sequence of the
CC VH or VL domain of 4D4, 4D4 H2-1 D11, 4D4com-2F9, 7F3, 71A10,
CC 2D23, 7F3com-2H2, 7F3com-3H5 or 7F3com-3D4; or a complementarity
CC determining region (CDR) having an amino acid sequence of a CDR of 4D4,
CC 4D4 H2-1 D11, 4D4com-2F9, 4D4com-2F9, 7F3, 71A10, 2D23, 7F3com-2H2,
CC 7F3com-3H5 or 7F3com-3D4. The antibody immunospecifically binds to a
CC human IL-9 polypeptide. Also described are: a pharmaceutical composition
CC comprising the IL-9 antibody and a carrier; a method for preventing,
CC treating, managing or ameliorating a disease or disorder characterised by
CC aberrant expression or activity of an IL-9 polypeptide or an IL-9R; a
CC method of diagnosing, prognosing, or monitoring a disorder or disease
CC characterised by aberrant expression or activity of an IL-9 polypeptide
CC or aberrant expression or activity of an IL-9R; a kit comprising the
CC antibody and instructions for use, in one or more containers; and an
CC article of manufacture comprising a packaging material and a
CC pharmaceutical agent contained within the packaging material, where the
CC pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9
CC antibody is useful in preparing a composition for diagnosing, treating or
CC preventing a disease or disorder characterised by aberrant expression or
CC activity of an IL-9 polypeptide or an IL-9R, e.g., respiratory infection or
CC caused by bacteria or respiratory syncytial virus, parainfluenza virus or
CC human metapneumovirus, inflammatory disorder such as asthma, allergy or
CC arthritis or autoimmune disorder such as rheumatoid arthritis and
CC multiple sclerosis. This is the amino acid sequence of a human IL-19
CC antibody variable heavy chain framework region 1.
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 120; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
RESULT 4
ADU80305
ID ADU80305 standard; peptide; 25 AA.
XX ADU80305;
AC ADU80305 (first entry)
XX 24-FEB-2005
DT Heavy chain framework region VHI DP7/21-2 FRL1.
DE Heavy chain framework region VHI DP7/21-2 FRL1.
XX cytostatic; gene therapy; antibody production; hematological disease;
KW immune disorder; neoplasm; b-cell lymphoma; framework region; FRL1.
XX Homo sapiens.
OS WO2004103404-A1.
PN 02-DEC-2004.
XX PS
XX 11-APR-2003; 2004US-0462259P.
PR 10-JUN-2003; 2003US-0477737P.
XX (MEDI-) MEDIMMUNE INC.
XX Reed JL;
XX WPI; 2004-775520/76.
XX New IL-9 antibody comprising a variable heavy or light domain or a
PT complementarity determining region having an amino acid sequence of e.g.,
PT 4D4, useful in treating or preventing e.g., respiratory infection or
PT inflammatory disorder.
XX Disclosure; SEQ ID NO 33; 291pp; English.
XX The invention describes a new IL-9 antibody comprising: a variable heavy
CC (VH) or variable light (VL) domain having an amino acid sequence of the
CC VH or VL domain of 4D4, 4D4 H2-1 D11, 4D4com-2F9, 7F3, 71A10,
CC 2D23, 7F3com-2H2, 7F3com-3H5 or 7F3com-3D4; or a complementarity
CC determining region (CDR) having an amino acid sequence of a CDR of 4D4,
CC 4D4 H2-1 D11, 4D4com-2F9, 4D4com-2F9, 7F3, 71A10, 2D23, 7F3com-2H2,
CC 7F3com-3H5 or 7F3com-3D4. The antibody immunospecifically binds to a
CC human IL-9 polypeptide. Also described are: a pharmaceutical composition
CC comprising the IL-9 antibody and a carrier; a method for preventing,
CC treating, managing or ameliorating a disease or disorder characterised by
CC aberrant expression or activity of an IL-9 polypeptide or an IL-9R; a
CC method of diagnosing, prognosing, or monitoring a disorder or disease
CC characterised by aberrant expression or activity of an IL-9 polypeptide
CC or aberrant expression or activity of an IL-9R; a kit comprising the
CC antibody and instructions for use, in one or more containers; and an
CC article of manufacture comprising a packaging material and a
CC pharmaceutical agent contained within the packaging material, where the
CC pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9
CC antibody is useful in preparing a composition for diagnosing, treating or
CC preventing a disease or disorder characterised by aberrant expression or
CC activity of an IL-9 polypeptide or an IL-9R, e.g., respiratory infection or
CC caused by bacteria or respiratory syncytial virus, parainfluenza virus or
CC human metapneumovirus, inflammatory disorder such as asthma, allergy or
CC arthritis or autoimmune disorder such as rheumatoid arthritis and
CC multiple sclerosis. This is the amino acid sequence of a human IL-19
CC antibody variable heavy chain framework region 1.
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 120; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
RESULT 5
ADY31444
ID ADY31444 standard; peptide; 25 AA.
XX ADY31444;
AC ADY31444 (first entry)
XX 05-MAY-2005
DT Human antibody heavy chain framework peptide - SEQ ID 276.
DE DNA library; humanized antibody; antibody engineering; heavy chain.
XX Homo sapiens.
OS US2005042664-A1.
PN 24-FEB-2005.
PD 20-AUG-2004; 2004US-00923068.
XX 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX (MEDI-) MEDIMMUNE INC.
XX Wu H, Dall-Acqua W, Damschroder M;
PI WPI; 2005-180802/19.
DR New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX Disclosure; SEQ ID NO 276; 179pp; English.
PS

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XX The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline heavy chain framework
CC peptide.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 120; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 6
ADY31447
ID ADY31447 standard; peptide; 25 AA.
XX
AC ADY31447;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 279.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
XX
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
XX encoding humanized heavy chain variable regions and humanized light chain
XX variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 279; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline heavy chain framework
CC peptide.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 120; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 7
ADY31453
ID ADY31453 standard; peptide; 25 AA.
XX
AC ADY31453;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 285.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
XX
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
XX encoding humanized heavy chain variable regions and humanized light chain
XX variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 285; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline heavy chain framework
CC peptide.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 120; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 8
ADY31459
ID ADY31459 standard; peptide; 25 AA.
XX
AC ADY31459;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 291.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
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RESULT 7
ADY31453
ID ADY31453 standard; peptide; 25 AA.
XX
AC ADY31453;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 285.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
XX
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
XX encoding humanized heavy chain variable regions and humanized light chain
XX variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 285; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline heavy chain framework
CC peptide.
XX
SQ Sequence 25 AA;

Query Match 100.0%; Score 120; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 8
ADY31459
ID ADY31459 standard; peptide; 25 AA.
XX
AC ADY31459;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 291.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
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KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgB; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX Homo sapiens.
 XX WO200183806-A1.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US014349.
 XX
 XX 02-MAY-2000; 2000US-00563222.
 XX
 XX (EPIC-) EPICYTE PHARM INC.
 XX
 XX Hiatt AC, Hein MB;
 XX WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 XX Disclosure; Fig 1B; 129pp; English.
 XX
 XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 CC IgB, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IgBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 XX Sequence 30 AA;
 SQ
 Query Match 100.0%; Score 120; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
 Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
 RESULT 14
 ADW87138
 ID ADW87138 standard; protein; 30 AA.
 XX
 XX ADW87138;
 XX
 XX 07-APR-2005 (first entry)
 XX
 XX Anti-human interleukin-13 antibody-associated protein #15.
 XX
 XX antibody engineering; antiasthmatic; dermatological; antiallergic;
 KW antinflammatory; gastrointestinal-gen.; cytostatic; immunostimulant;
 KW diagnosis; interleukin-13; heavy chain variable region;
 KW light chain variable region; complementarity determining region; asthma;
 KW atopic dermatitis; allergic rhinitis; fibrosis;
 KW inflammatory bowel disease; Hodgkins disease.
 XX
 XX Homo sapiens.

XX
 PN CB2403952-A.
 XX
 PD 19-JAN-2005.
 XX
 XX 15-JUL-2004; 2004GB-00015857.
 XX
 XX 15-JUL-2003; 2003US-0487512P.
 PR 31-MAR-2004; 2004GB-00007315.
 PR 31-MAR-2004; 2004US-0558216P.
 PR 24-MAY-2004; 2004US-0573791P.
 XX
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Monk PD, Jermutus L, Minter RR, Shorrock CP;
 XX WPI; 2005-104209/12.
 XX
 XX Novel isolated specific binding molecule for human interleukin-13, having
 PT antibody antigen-binding domain site composed of human variable heavy and
 PT light chain domains with complementarity determining regions, useful for
 PT treating asthma.
 XX
 XX Disclosure; SEQ ID NO 27; 192pp; English.
 XX
 XX The invention relates to an isolated specific binding molecule (I) for
 CC human interleukin (IL)-13, comprising an antibody antigen-binding domain
 CC site composed of human antibody VH and VL domain comprising a set of
 CC complementarity determining regions (CDR's) HCDR1, HCDR2, HCDR3, LCDR1,
 CC LCDR2 and LCDR3. (I) is useful for in vitro binding of (I) to human IL-13
 CC or its fragment, and further involves determining the amount of binding
 CC of (I) to IL-13 or its fragment. (I) is useful in the manufacture of a
 CC medicament for treatment of a disease or disorder chosen from asthma,
 CC atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel
 CC disease and Hodgkin's lymphoma. (I) is useful in diagnosing diseases such
 CC as asthma, atopic dermatitis, in the subject. (I) preferably neutralizes
 CC human IL-13. This sequence corresponds to protein used in the invention.
 XX
 XX Sequence 30 AA;
 SQ
 Query Match 100.0%; Score 120; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
 Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
 RESULT 15
 ADX01239
 ID ADX01239 standard; peptide; 30 AA.
 XX
 XX ADX01239;
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Humanized antibody generation peptide #10.
 XX
 XX antibody engineering; antibody production; immunosuppressive;
 KW immunotherapy; heavy chain variable region; light chain variable region;
 KW graft rejection; graft versus host disease; autoimmune disease.
 XX
 XX Rattus sp.
 OS
 XX US6849258-B1.
 PN
 XX 01-FEB-2005.
 XX
 XX 26-JUN-2000; 2000US-00462140.
 PF
 XX 07-JUN-1995; 95US-00472281.
 XX
 XX 18-JUL-1997; 97WO-US012645.
 PR

```

XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
PA (BIOT-) BIOTRANSPLANT INC.
XX
PI Bazin H, Latinne D, Kaplan R, Kieber-Emmons T, Postema CE;
PI White-Scharf ME;
XX
DR WPI; 2005-129962/14.
XX
PT New humanized antibody comprising the complementary determining regions
PT (CDRs) from LO-CD2a, useful for preventing or inhibiting graft rejection,
PT graft versus host disease or autoimmune disease.
XX
PS Example 7; SEQ ID NO 52; 126pp; English.
XX
CC The invention relates to a humanized antibody comprising the CDRs from LO
CC -CD2a, produced by the cell line deposited as American Type Culture
CC Collection (ATCC) HB11423, the humanized antibody containing in the
CC framework of the heavy chain variable region of the humanized antibody,
CC amino acids 47, 67, 70, 72, 75, 85, and 87, and one, two, three, or four of
CC amino acids 12, 13, 28, and 48 of the rat LO-CD2a heavy chain variable
CC region of 118 amino acids, fully defined in the specification. The
CC antibody is useful for preventing or inhibiting graft rejection, graft
CC versus host disease or autoimmune disease. This sequence corresponds to a
CC peptide used in the invention.
XX
SQ Sequence 30 AA;
Query Match 100.0%; Score 120; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Search completed: April 25, 2006, 06:15:07
Job time : 136.491 secs

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:15:41 ; Search time 21.2264 Seconds
(without alignments)
113.322 Million cell updates/sec

Title: US-10-764-428-1

Perfect score: 120

Sequence: 1 QVQLVQSGAEVKKPGASVKVSKAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	98	2 S26910	Ig heavy chain V r
2	120	100.0	98	2 S26920	Ig heavy chain V r
3	120	100.0	98	2 S26918	Ig heavy chain V r
4	120	100.0	98	2 S26912	Ig heavy chain V r
5	120	100.0	98	2 S26938	Ig heavy chain V r
6	120	100.0	98	2 S26913	Ig heavy chain V r
7	120	100.0	98	2 S26919	Ig heavy chain V r
8	120	100.0	104	2 S69899	Ig heavy chain V r
9	120	100.0	111	2 S21925	Ig heavy chain V r
10	120	100.0	116	2 S31667	Ig heavy chain pre
11	120	100.0	117	1 HVHU35	Ig heavy chain pre
12	120	100.0	117	1 HVHUHG	Ig heavy chain pre
13	120	100.0	117	2 S18552	Ig heavy chain V r
14	120	100.0	117	2 S31680	Ig heavy chain V r
15	120	100.0	117	2 S18553	Ig heavy chain V r
16	120	100.0	117	2 S18551	Ig heavy chain V r
17	120	100.0	118	2 S36265	Ig heavy chain V r
18	120	100.0	122	2 S36271	Ig heavy chain V r
19	120	100.0	124	2 S19665	Ig heavy chain V r
20	120	100.0	129	2 S46393	Ig heavy chain V r
21	120	100.0	132	2 S31596	Ig heavy chain V r
22	120	100.0	135	2 S49530	anti-Sm antibody V
23	120	100.0	142	2 A32483	Ig heavy chain V r
24	120	100.0	148	2 S25257	Ig heavy chain V r
25	118	98.3	127	2 S34014	Ig heavy chain V r
26	117	97.5	98	2 A30523	Ig heavy chain V-I
27	117	97.5	98	2 S26915	Ig heavy chain V r
28	117	97.5	98	2 S24680	Ig heavy chain V1
29	117	97.5	98	2 S46463	Ig heavy chain V1

ALIGNMENTS

RESULT 1

S26910

Ig heavy chain V region (DP-1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S26910

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26910

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI00001163FA; EMBL:Z12303; NID:G32847; PIDN:CAA78173.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.9e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25

Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 2

S26920

Ig heavy chain V region (DP-7) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26920

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26920

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI00001163FE; EMBL:Z12309; NID:G32958; PIDN:CAA78179.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.9e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25

```
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25
|||||
RESULT 3
S26918
Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 4
S26912
Ig heavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI00001163FF; EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 5
S26938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
```

```
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI000011644A; EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 6
S26913
Ig heavy chain V region (DP-12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26913
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116400; EMBL:Z12314; NID:g32852; PIDN:CAA78184.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 7
S26919
Ig heavy chain V region (DP-14) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26919
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F31; EMBL:Z12316; NID:g32855; PIDN:CAA78186.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 8
S26919
Ig heavy chain V region (DP-14) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26919
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F31; EMBL:Z12316; NID:g32855; PIDN:CAA78186.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db      1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 8
```

S69899
Ig heavy chain V region (clone RPT57H), rheumatoid factor - human
C/Species: Homo sapiens (man)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69899
R/Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J.
Eur. J. Immunol. 23, 1220-1225, 1993
A/Title: Synovial Igg rheumatoid factors show evidence of an antigen-driven immune response
A/Reference number: S69896; MUID:93272805; PMID:8500520
A/Accession: S69899
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-104 <RAN>
A/Cross-references: UNIPARC:UPI000011664P; EMBL:Z34893; NID:9509803; PIDN:CAA84376.1; P1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 9
S21925
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S21925
R/Friedman, D.F.
submitted to the EMBL Data Library, July 1991
A/Reference number: S21923
A/Accession: S21925
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-111 <FRI>
A/Cross-references: UNIPARC:UPI0000115FAL; EMBL:X60503; NID:933626; PIDN:CAA43023.1; P1D
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 120; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSCKAS 44

RESULT 10
S31667
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31667
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the;
A/Reference number: S31585
A/Accession: S31667
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <CUI>
A/Cross-references: UNIPARC:UPI000011647P; EMBL:Z14215; NID:937799; PIDN:CAA78584.1; P1D
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 19 QVQLVQSGAEVKKPGASVKVSCKAS 43

RESULT 11
HVHJ35
Ig heavy chain precursor V region (V25) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S00476; S34013
R/Matauda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuha
EMBO J. 7, 1047-1051, 1988
A/Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain lo
A/Reference number: S00476; MUID:88296408; PMID:2841108
A/Accession: S00476
A/Molecule type: DNA
A/Residues: 1-117 <MATS>
A/Cross-references: UNIPROT:P23083; UNIPARC:UPI00001179DB; EMBL:X07448; NID:933104; PIDN
A/Note: the authors translated the codon AGT for residue 89 as Met
R/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:93209281; PMID:7681398
A/Accession: S34013
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 20-116 <MAR>
A/Cross-references: UNIPARC:UPI000017372B
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (V25) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSCKAS 44

RESULT 12
HVHJHG
Ig heavy chain precursor V-I region (HG3) - human
C/Species: Homo sapiens (man)
C/Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C/Accession: A02024
R/Rechavi, G.; Ram, D.; Glazer, L.; Zakut, R.; Givol, D.
Proc. Natl. Acad. Sci. U.S.A. 80, 855-859, 1983
A/Title: Evolutionary aspects of immunoglobulin heavy chain variable region (V-H) gene
A/Reference number: A02024; MUID:83144028; PMID:6298778
A/Accession: A02024
A/Molecule type: DNA
A/Residues: 1-117 <REC>
A/Cross-references: UNIPROT:P01743; UNIPARC:UPI000012CER1
A/Note: the sequence was determined from the germline gene
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
A/Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V-I region (HG3) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44
|||||

RESULT 13
S18552
Ig heavy chain V region precursor (VI-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18552
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18552
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <SHI>
A;Cross-references: UNIPARC:UPI0000115FEB; EMBL:X62107; NID:g37833; PIDN:CAA44017.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44
|||||

RESULT 14
S31680
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CU>
A;Cross-references: UNIPARC:UPI000011647D; EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44
|||||

Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44
|||||

RESULT 15
S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18553; S26916
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18553
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <SHI>
A;Cross-references: UNIPARC:UPI0000176E84; EMBL:X62109
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26985; MUID:93021117; PMID:1404388
A;Accession: S26916
A;Molecule type: DNA
A;Residues: 20-117 <TOM>
A;Cross-references: UNIPARC:UPI0000116402; EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 120; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44
|||||

Search completed: April 25, 2006, 06:26:11
Job time : 21.2264 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 133,491 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-1

Perfect score: 120

Sequence: 1 QVQLVQSGAEVKPKGASVKVCKAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	117	1 HV1B_HUMAN	P21743 homo sapien
2	120	100.0	117	1 HV1G_HUMAN	P23083 homo sapien
3	120	100.0	159	2 Q96QSO_HUMAN	Q96QSO homo sapien
4	120	100.0	500	2 Q6N091_HUMAN	Q6N091 homo sapien
5	117	97.5	117	1 HV1A_HUMAN	P01742 homo sapien
6	117	97.5	120	2 Q6NSA4_HUMAN	Q6NSA4 homo sapien
7	117	97.5	480	2 Q6PJF1_HUMAN	Q6PJF1 homo sapien
8	117	97.5	498	2 Q6N041_HUMAN	Q6N041 homo sapien
9	116	96.7	150	2 Q9Y298_HUMAN	Q9Y298 homo sapien
10	114	95.0	119	2 Q9UL94_HUMAN	Q9UL94 homo sapien
11	114	95.0	124	2 Q9UL92_HUMAN	Q9UL92 homo sapien
12	114	95.0	125	2 Q9UL95_HUMAN	Q9UL95 homo sapien
13	114	95.0	244	2 Q6SZC8_HUMAN	Q6SZC8 homo sapien
14	113	94.2	52	2 Q6QQR9_HUMAN	Q6QQR9 homo sapien
15	112	93.3	480	2 Q6P089_HUMAN	Q6P089 homo sapien
16	112	93.3	519	2 Q5EBM2_HUMAN	Q5EBM2 homo sapien
17	111	92.5	119	2 Q9GY22_MOUSE	Q9GY22 mus musculu
18	110	91.7	125	1 Q6PIL0_HUMAN	Q6PIL0 homo sapien
19	110	91.7	147	1 HV1C_HUMAN	P01744 homo sapien
20	109	90.8	518	2 Q6N030_HUMAN	Q6N030 homo sapien
21	108	90.0	469	2 Q727P5_HUMAN	Q727P5 homo sapien
22	107	89.2	124	1 HV1D_HUMAN	P01760 homo sapien
23	107	89.2	124	1 HV1B_HUMAN	P01761 homo sapien
24	107	89.2	157	2 Q59J78_HUMAN	Q59J78 homo sapien
25	105	87.5	477	2 Q59B1_RAT	Q59B1 rattus norv
26	104	86.7	475	2 Q6N095_HUMAN	Q6N095 homo sapien
27	103	85.8	125	1 HV1F_HUMAN	P06326 homo sapien
28	103	85.8	473	2 Q9D8L4_MOUSE	Q9D8L4 mus musculu
29	103	85.8	496	2 Q96DK0_HUMAN	Q96DK0 homo sapien
30	103	85.8	506	2 Q6WZM0_HUMAN	Q6WZM0 homo sapien
31	102	85.0	484	2 Q99LA6_MOUSE	Q99LA6 mus musculu

32	102	85.0	497	2 Q8WY24_HUMAN	Q8WY24 homo sapien
33	102	85.0	617	2 Q4KML5_MOUSE	Q4KML5 mus musculu
34	101	84.2	168	2 Q8VDC9_MOUSE	Q8VDC9 mus musculu
35	101	84.2	208	2 Q6ZP87_HUMAN	Q6ZP87 homo sapien
36	101	84.2	458	2 Q5BK05_RAT	Q5BK05 rattus norv
37	101	84.2	458	2 Q6PJ22_MOUSE	Q6PJ22 mus musculu
38	101	84.2	475	2 Q5FVPT1_RAT	Q5FVPT1 rattus norv
39	101	84.2	481	2 Q91WT1_MOUSE	Q91WT1 mus musculu
40	101	84.2	591	2 Q4QQW0_RAT	Q4QQW0 rattus norv
41	101	84.2	613	2 Q8VCX7_MOUSE	Q8VCX7 mus musculu
42	100	83.3	458	2 Q5BJ22_RAT	Q5BJ22 rattus norv
43	100	83.3	485	2 Q58B61_MOUSE	Q58B61 mus musculu
44	99	82.5	116	2 Q9UL89_HUMAN	Q9UL89 homo sapien
45	98	81.7	111	2 Q9D9B8_MOUSE	Q9D9B8 mus musculu

ALIGNMENTS

RESULT 1

ID	HV1B_HUMAN	STANDARD	PRT	117 AA
AC	P01743;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig heavy chain V-I region HG3 precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
EN	[1]			
RP	NUCLEOTIDE SEQUENCE			
RX	MEDLINE=83144028; PubMed=6298778;			
RA	Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;			
RT	"Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups."			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).			
CC	-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL; J00240; AAA52988.1; -; Genomic_DNA.			
DR	PIR; A02024; HVHUG.			
DR	HSSP; P01751; 1NOB.			
DR	SMR; P01743; 20-116.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
DR	Immunoglobulin domain; Immunoglobulin V region; Signal.			
KW	SIGNAL 1 19			
FT	CHAIN 20 117			
FT	DOMAIN 20 >117			
FT	NON_TER 117 117			
FT	SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;			
SQ				

Query Match 100.0%; Score 120; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKAS 25

DB 20 QVQLVQSGAEVKPKGASVKVCKAS 44

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RESULT 2
HVIG HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -; mRNA.
DR HSSP; P01869; 1AE6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
Query Match 100.0%; Score 120; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
DB 20 QVQLVQSGAEVKKPGASVKVSCKAS 44
|||||
RESULT 4
Q6N091_HUMAN
ID Q6N091_HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N091;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C0220 (Fragment).
GN Name=DKFZp686C0220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640625; CAB45779.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMART; P01751; 270-478.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
Query Match 100.0%; Score 120; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
|||||
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; S00476; HVHU35.
DR HSSP; P01751; 1NOB.
DR SMR; P23083; 20-117.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117 Ig heavy chain V-I region V35.
FT DOMAIN 20 >117 Ig-like.
FT NON TER 117
FT NON TER 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
Query Match 100.0%; Score 120; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
DB 20 QVQLVQSGAEVKKPGASVKVSCKAS 44
|||||
RESULT 3
Q6QSO_HUMAN
ID Q6QSO_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q6QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -; mRNA.
DR HSSP; P01869; 1AE6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
Query Match 100.0%; Score 120; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
DB 20 QVQLVQSGAEVKKPGASVKVSCKAS 44
|||||
RESULT 4
Q6N091_HUMAN
ID Q6N091_HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N091;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C0220 (Fragment).
GN Name=DKFZp686C0220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640625; CAB45779.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMART; P01751; 270-478.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
Query Match 100.0%; Score 120; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
|||||
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016381; AAH16381.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;

Query Match 97.5%; Score 117; DB 2; Length 480;
Best Local Similarity 96.0%; Pred. No. 1.5e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 20 QVQLVQSGAEVKKPGSSVKVSCKAS 44
|||||:|||||:|||||:|||||:|||||:
[1]

RESULT 8
Q6N041 HUMAN
ID Q6N041 HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Names=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Oeang A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BX640710; CAB45829.1; -; mRNA.

Query Match 97.5%; Score 117; DB 2; Length 480;
Best Local Similarity 96.0%; Pred. No. 1.5e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 20 QVQLVQSGAEVKKPGSSVKVSCKAS 44
|||||:|||||:|||||:|||||:|||||:
[1]

RESULT 9
Q9Y298 HUMAN
ID Q9Y298 HUMAN PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN Name=IGG VH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jacquemin M.G., Vander Elst L.P.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224083; CAA11829.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR SMR; Q9Y298; 20-149.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

Query Match 96.7%; Score 116; DB 2; Length 150;
Best Local Similarity 96.0%; Pred. No. 6.5e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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DR HSSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IGV; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER.
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 97.5%; Score 117; DB 2; Length 498;
Best Local Similarity 96.0%; Pred. No. 1.5e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 35 QVQLVQSGADVKKPGASVKVSCKAS 59
|||||:|||||:|||||:|||||:|||||:
[1]

RESULT 9
Q9Y298 HUMAN
ID Q9Y298 HUMAN PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN Name=IGG VH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT Igg4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Vander Elst L.P.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224083; CAA11829.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR SMR; Q9Y298; 20-149.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

Query Match 96.7%; Score 116; DB 2; Length 150;
Best Local Similarity 96.0%; Pred. No. 6.5e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
|||||:|||||:|||||:|||||:|||||:
[1]
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Db 20 QVQLVQSGAEVKKPGASVKVCKAS 44

RESULT 10

ID Q9UL94 HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94; 119 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13864F5345F4A16E CRC64;

Query Match 95.0%; Score 114; DB 2; Length 119;
Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVCKAS 25

Db 1 EVQLVESGAEVKKPGASVKVCKAS 25

RESULT 11

ID Q9UL92 HUMAN PRELIMINARY; PRT; 124 AA.
AC Q9UL92; 124 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -; mRNA.
DR HSSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 124

SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 95.0%; Score 114; DB 2; Length 124;
Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVCKAS 25

Db 1 EVQLVESGAEVKKPGASVKVCKAS 25

RESULT 12

ID Q9UL95 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q9UL95; 125 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 95.0%; Score 114; DB 2; Length 125;
Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVCKAS 25

Db 1 EVQLVESGAEVKKPGASVKVCKAS 25

RESULT 13

ID Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8; 244 AA.
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;

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RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 95.0%; Score 114; DB 2; Length 244;
Best Local Similarity 96.0%; Pred. No. 2.2e-09;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 14
Q96QR9 HUMAN
ID Q96QR9 HUMAN PRELIMINARY; PRT; 52 AA.
AC Q96QR9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039026; AAK82650.1; -; mRNA.
DR HSP; P01750; IQNZ.
DR Ensembl; ENSG00000153613; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5560 MW; 83875B1D18CB976 CRC64;

Query Match 94.2%; Score 113; DB 2; Length 52;
Best Local Similarity 96.0%; Pred. No. 6.6e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44

RESULT 15
Q6P089 HUMAN
ID Q6P089 HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6P089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Straussberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065733; AAH65733.1; -; mRNA.
DR HSP; P01751; 1A6W.
DR SNR; Q6P089; 250-458.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;

Query Match 93.3%; Score 112; DB 2; Length 480;
Best Local Similarity 96.0%; Pred. No. 9e-09;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 20 QVQLVQSGAEVKKPGASVKVSKAS 44

Search completed: April 25, 2006, 06:24:39
Job time : 135.491 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 33.7264 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-1

Perfect score: 120

Sequence: 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgm2_6/ptodata/1/iaa/6-COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/H-COMB.pep.*
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6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	30	1 US-07-946-421-11	Sequence 11, Appl
2	120	100.0	30	1 US-08-477-877B-52	Sequence 52, Appl
3	120	100.0	30	1 US-08-137-117D-146	Sequence 146, App
4	120	100.0	30	1 US-08-137-117D-152	Sequence 152, App
5	120	100.0	30	1 US-08-137-117D-157	Sequence 157, App
6	120	100.0	30	1 US-08-472-281A-52	Sequence 52, Appl
7	120	100.0	30	1 US-08-436-717-146	Sequence 146, App
8	120	100.0	30	1 US-08-436-717-152	Sequence 152, App
9	120	100.0	30	1 US-08-436-717-157	Sequence 157, App
10	120	100.0	30	1 US-08-477-989B-52	Sequence 52, Appl
11	120	100.0	30	1 US-08-569-147-54	Sequence 54, Appl
12	120	100.0	30	2 US-09-563-222C-133	Sequence 133, App
13	120	100.0	30	2 US-09-830-748B-37	Sequence 37, Appl
14	120	100.0	30	2 US-09-462-140D-52	Sequence 52, Appl
15	120	100.0	44	2 US-09-269-921-133	Sequence 133, App
16	120	100.0	87	1 US-08-497-312-16	Sequence 16, Appl
17	120	100.0	87	2 US-09-254-180C-150	Sequence 150, App
18	120	100.0	87	2 US-09-254-180C-152	Sequence 152, App
19	120	100.0	88	2 US-09-254-180C-151	Sequence 151, App
20	120	100.0	96	2 US-10-330-613A-54	Sequence 54, Appl
21	120	100.0	97	1 US-08-290-592E-16	Sequence 16, Appl
22	120	100.0	97	4 PCT-US95-10053-13	Sequence 13, Appl
23	120	100.0	97	4 PCT-US96-09448-16	Sequence 16, Appl
24	120	100.0	98	2 US-10-194-975-1	Sequence 1, Appl
25	120	100.0	98	2 US-10-194-975-2	Sequence 2, Appl
26	120	100.0	98	2 US-10-194-975-4	Sequence 4, Appl
27	120	100.0	98	2 US-10-194-975-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-07-946-421-11
; Sequence 11, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Region
; LOCATION: 30
; OTHER INFORMATION: /note= "Amino acid 30 can be Thr or

Sequence 53, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 5, Appl
Sequence 75, Appl
Sequence 41, Appl
Sequence 17, Appl
Sequence 90, Appl
Sequence 91, Appl
Sequence 96, Appl
Sequence 105, App
Sequence 128, App
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 90, Appl

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117D
;; FILING DATE: 20-DEC-1993
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 152:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-137-117D-152

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 5
US-08-137-117D-157
; Sequence 157, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117D
;; FILING DATE: 20-DEC-1993
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 157:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-137-117D-157

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 6
US-08-472-281A-52
; Sequence 52, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latime, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-08-472-281A-52

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 7
US-08-436-717-146
; Sequence 146, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-436-717-152

; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-436-717-146

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSKAS 25

RESULT 8
US-08-436-717-152
; Sequence 152, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-436-717-152
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Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKPGASVKVSCKAS 25

RESULT 9
US-08-436-717-157
; Sequence 157, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-436-717-157

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKPGASVKVSCKAS 25

RESULT 10
US-08-477-989B-52
; Sequence 52, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina B.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-989B-52

Query Match 100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKPGASVKVSCKAS 25

RESULT 11
US-08-569-147-54
; Sequence 54, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES

Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 15
US-09-269-921-133
; Sequence 133, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: HG3
; PUBLICATION INFORMATION:
; AUTHORS: Rechavi, G. et al.
; JOURNAL: PROC. NATL. ACAD. SCI. USA
; VOLUME: 80
; PAGES: 855-859
; DATE: 1983
US-09-269-921-133

Query Match 100.0%; Score 120; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

Search completed: April 25, 2006, 06:28:39
Job time : 34.7264 secs

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; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-253-33

Query Match      100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 3
US-10-849-615-95
; Sequence 95, Application US/10849615
; Publication No. US20050025764A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Julian
; APPLICANT: Marquis, David M.
; APPLICANT: Ondek, Brian
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: CD20 BINDING MOLECULES
; FILE REFERENCE: AME-09016
; CURRENT APPLICATION NUMBER: US/10/849,615
; CURRENT FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(25)
; OTHER INFORMATION: FRH1 VKI (DP7/21-2)
US-10-849-615-95

Query Match      100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 4
US-10-923-068-276
; Sequence 276, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-276

Query Match      100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 5
US-10-923-068-279
; Sequence 279, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-279

Query Match      100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 6
US-10-923-068-285
; Sequence 285, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-285

Query Match      100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 7
US-10-923-068-291
; Sequence 291, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
```


; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 291
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-291

Query Match 100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 8
US-10-923-068-300
; Sequence 300, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-300

Query Match 100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 9
US-10-823-810-33
; Sequence 33, Application US/10823810
; Publication No. US20050147607A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
; FILE REFERENCE: 10271-113-999
; CURRENT APPLICATION NUMBER: US/10/823,810
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,307
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,801
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-810-33

Query Match 100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 10
US-09-949-559-95
; Sequence 95, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework H1
US-09-949-559-95

Query Match 100.0%; Score 120; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 11
US-09-875-221A-95
; Sequence 95, Application US/09875221A
; Publication No. US20030028605A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework H1
US-09-875-221A-95

Query Match 100.0%; Score 120; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds
(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-1

Perfect score: 120

Sequence: 1 QVQLVQSGAEVKPGASVKVSKAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SID55/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SID55/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 5: /SID55/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 6: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /SID55/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	25	US-11-105-268-33	Sequence 33, Appl
2	120	100.0	30	US-11-108-135-4	Sequence 4, Appl
3	120	100.0	30	US-11-004-590-111	Sequence 11, App
4	120	100.0	30	US-11-126-978-4	Sequence 4, Appl
5	120	100.0	30	US-11-226-886-48	Sequence 48, Appl
6	120	100.0	44	US-11-226-325-137	Sequence 137, App
7	120	100.0	87	US-11-226-325-200	Sequence 200, App
8	120	100.0	98	US-11-054-669-1	Sequence 1, Appl
9	120	100.0	98	US-11-054-669-2	Sequence 2, Appl
10	120	100.0	98	US-11-054-669-3	Sequence 3, Appl
11	120	100.0	98	US-11-054-669-4	Sequence 4, Appl
12	120	100.0	98	US-11-054-669-7	Sequence 7, Appl
13	120	100.0	98	US-11-084-554-15	Sequence 15, Appl
14	120	100.0	98	US-11-084-554-16	Sequence 16, Appl
15	120	100.0	98	US-11-084-554-18	Sequence 18, Appl
16	120	100.0	98	US-11-084-554-20	Sequence 20, Appl
17	120	100.0	98	US-11-061-848-17	Sequence 17, Appl
18	120	100.0	98	US-11-004-590-1	Sequence 1, Appl
19	120	100.0	98	US-11-004-590-2	Sequence 2, Appl
20	120	100.0	98	US-11-004-590-3	Sequence 3, Appl
21	120	100.0	98	US-11-004-590-4	Sequence 4, Appl
22	120	100.0	98	US-11-004-590-7	Sequence 7, Appl
23	120	100.0	98	US-11-136-250-15	Sequence 15, Appl
24	120	100.0	98	US-11-136-250-16	Sequence 16, Appl
25	120	100.0	98	US-11-136-250-18	Sequence 18, Appl

26 120 100.0 98 7 US-11-136-250-20 Sequence 20, Appl
27 120 100.0 99 7 US-11-084-554-23 Sequence 23, Appl
28 120 100.0 99 7 US-11-136-250-23 Sequence 23, Appl
29 120 100.0 109 7 US-11-155-843-50 Sequence 50, Appl
30 120 100.0 109 7 US-11-155-843-51 Sequence 51, Appl
31 120 100.0 109 7 US-11-155-843-52 Sequence 52, Appl
32 120 100.0 109 7 US-11-155-843-53 Sequence 53, Appl
33 120 100.0 109 7 US-11-155-843-56 Sequence 56, Appl
34 120 100.0 109 7 US-11-155-843-83 Sequence 83, Appl
35 120 100.0 109 7 US-11-155-843-84 Sequence 84, Appl
36 120 100.0 109 7 US-11-155-843-85 Sequence 85, Appl
37 120 100.0 109 7 US-11-155-843-86 Sequence 86, Appl
38 120 100.0 109 7 US-11-155-843-89 Sequence 89, Appl
39 120 100.0 113 7 US-11-177-648-11 Sequence 11, Appl
40 120 100.0 113 7 US-11-177-648-12 Sequence 12, Appl
41 120 100.0 113 7 US-11-177-648-13 Sequence 13, Appl
42 120 100.0 113 7 US-11-177-648-16 Sequence 16, Appl
43 120 100.0 113 7 US-11-177-648-77 Sequence 77, Appl
44 120 100.0 113 7 US-11-177-648-85 Sequence 85, Appl
45 120 100.0 113 7 US-11-177-648-86 Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-11-105-268-33
; Sequence 33, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allnan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-33

Query Match 100.0%; Score 120; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSKAS 25

Db 1 QVQLVQSGAEVKPGASVKVSKAS 25

RESULT 2

US-11-108-135-4
; Sequence 4, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuailon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21


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; SEQ ID NO 137
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the H chain V region (1) HG3
US-11-226-325-137

Query Match      100.0%; Score 120; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 7
US-11-226-325-200
; Sequence 200, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/11/226,325
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/509,098
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Design of V
; OTHER INFORMATION: region of Natural Humanized Antibody (HG3)
US-11-226-325-200

Query Match      100.0%; Score 120; DB 7; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
   |||||
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 8
US-11-054-669-1
; Sequence 1, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-3

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; ORGANISM: Homo sapiens
US-11-054-669-1

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 9
US-11-054-669-2
; Sequence 2, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-2

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
   |||||
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25

RESULT 10
US-11-054-669-3
; Sequence 3, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-3

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
   |||||
Db 1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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RESULT 11
US-11-054-669-4
; Sequence 4, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-4

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Db      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||

RESULT 12
US-11-054-669-7
; Sequence 7, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-7

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||
Db      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||

RESULT 13
US-11-084-554-15
; Sequence 15, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-15

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||
Db      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||

RESULT 14
US-11-084-554-16
; Sequence 16, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-16

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Db      1 QVQLVQSGAEVKKPGASVKVSCKAS 25
      |||||

RESULT 15
US-11-084-554-18
; Sequence 18, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
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; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-18

Query Match      100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
Db      1 QVQLVQSGAEVKKPGASVKVSCKAS 25

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Job time : 16.2044 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 133.491 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-2

Perfect score: 124
Sequence: 1 QVQLQSGPGLVKPSQTLTLCTVTS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124	100.0	25	8	Adq90698 Anti-VEGF
2	124	100.0	25	9	Ady31549 Human ant
3	124	100.0	30	5	Abg98300 Human ant
4	124	100.0	30	5	Abg98301 Human ant
5	124	100.0	30	5	Aau70466 Human hea
6	124	100.0	30	9	Ady31417 Human ant
7	124	100.0	30	9	Aea21493 Human ant
8	124	100.0	30	9	Aea21457 Human ant
9	124	100.0	95	7	Adc99829 Anti-huma
10	124	100.0	95	7	Adc99829 Anti-MUC1
11	124	100.0	95	7	Adf09871 Anti-MUC1
12	124	100.0	98	7	Adc99849 Anti-huma
13	124	100.0	98	7	Adc99849 Anti-MUC1
14	124	100.0	98	7	Adf09891 Anti-MUC1
15	124	100.0	99	5	Abg78215 Human Fv
16	124	100.0	99	5	Abg91906 Human ant
17	124	100.0	99	6	Abc27105 Human ger
18	124	100.0	99	6	Abc27103 Human ger
19	124	100.0	99	6	Abc27106 Human ger
20	124	100.0	99	7	Adc99848 Germline
21	124	100.0	99	7	Adc99817 Anti-huma
22	124	100.0	99	7	Adc99844 Germline
23	124	100.0	99	7	Adc99836 Germline
24	124	100.0	99	7	Adc99816 Germline

25	124	100.0	99	7	Adc99828	Germline
26	124	100.0	99	7	Adc99828	Anti-MUC1
27	124	100.0	99	7	Adc99828	Anti-MUC1
28	124	100.0	99	7	Adc99828	Anti-MUC1
29	124	100.0	99	7	Adc99828	Anti-MUC1
30	124	100.0	99	7	Adc99828	Anti-MUC1
31	124	100.0	99	7	Adc99828	Anti-MUC1
32	124	100.0	99	7	Adc99828	Anti-MUC1
33	124	100.0	99	7	Adc99828	Anti-MUC1
34	124	100.0	99	7	Adc99828	Anti-MUC1
35	124	100.0	99	7	Adc99828	Anti-MUC1
36	124	100.0	99	7	Adc99828	Anti-MUC1
37	124	100.0	99	7	Adc99828	Anti-MUC1
38	124	100.0	99	7	Adc99828	Anti-MUC1
39	124	100.0	99	7	Adc99828	Anti-MUC1
40	124	100.0	99	7	Adc99828	Anti-MUC1
41	124	100.0	99	7	Adc99828	Anti-MUC1
42	124	100.0	99	7	Adc99828	Anti-MUC1
43	124	100.0	99	7	Adc99828	Anti-MUC1
44	124	100.0	99	7	Adc99828	Anti-MUC1
45	124	100.0	99	7	Adc99828	Anti-MUC1

ALIGNMENTS

RESULT 1

Adq90698
ID ADQ90698 standard; peptide; 25 AA.

XX AC ADQ90698;

XX AC ADQ90698;

DT 21-OCT-2004 (first entry)

XX AC ADQ90698;

DE DE Anti-VEGF antibody heavy chain FRI subgroup II peptide SEQ ID NO:2.

XX AC ADQ90698;

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XX AC ADQ90698;

XX AC ADQ90698;

CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents a heavy chain FRI peptide of an anti-VEGF (vascular
 CC endothelial cell growth factor) antibody, which is used in the
 CC exemplification of the present invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 124; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.8e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 |||||
 Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 2

ADY31549
 ID ADY31549 standard; peptide; 25 AA.

AC ADY31549;

DT 05-MAY-2005 (first entry)

XX Human antibody heavy chain framework peptide - SEQ ID 381.

XX DNA library; humanized antibody; antibody engineering; heavy chain.

XX Homo sapiens.

XX US2005042664-A1.

XX 24-FEB-2005.

XX 20-AUG-2004; 2004US-00923068.

XX 22-AUG-2003; 2003US-0497213P.

XX 13-OCT-2003; 2003US-0510741P.

XX (MEDI-) MEDIMUNE INC.

XX Wu H, Dall-Acqua W, Damschroder M;

XX WPI; 2005-180802/19.

XX New library of nucleic acid sequences comprises nucleotide sequences
 XX encoding humanized heavy chain variable regions and humanized light chain
 XX variable regions, useful for producing humanized antibodies.

XX Disclosure; SEQ ID NO 381; 179pp; English.

XX The invention comprises a library of nucleotide sequences encoding
 XX humanized antibody heavy chain variable regions and humanized antibody
 XX light chain variable regions. The library of the invention is useful for
 XX producing humanized antibodies, or for re-engineering or reshaping an
 XX antibody from a first species for use in a second species. The present
 XX amino acid sequence represents a human germline heavy chain framework
 XX peptide.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 124; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.8e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 |||||
 Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 3

ABG98300
 ID ABG98300 standard; peptide; 30 AA.

XX AC ABG98300;

XX 08-JAN-2003 (first entry)

XX Human antibody Z18320 (Genbank) kappa chain variable region FR1.

XX Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40;
 XX T-cell activation; B-cell differentiation; framework region;
 XX cellular immune response; gene therapy; graft rejection; human; FR;
 XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
 XX asthma; multiple sclerosis; allergy; diabetes mellitus;
 XX systemic lupus erythematosus; graft-versus-host disease.

XX Homo sapiens.

XX WO200194586-A2.

XX 13-DEC-2001.

XX 06-JUN-2001; 2001WO-US018098.

XX 06-JUN-2000; 2000US-0209584P.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;

XX WPI; 2002-188261/24.

XX New antibodies binding to an epitope on gp39, useful for preventing graft
 XX rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or
 XX multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
 XX disease).

XX Disclosure; Page 47; 130pp; English.

XX The invention relates to an antibody which binds to an epitope on gp39,
 XX is new, where the epitope is distinct from the epitope bound by IDEC-131,
 XX and the antibody has a non-agonistic effect on T-cell activation and
 XX inhibits gp39/CD40 interaction. Also included are: (1) an improved method
 XX of treating a disease by modulating gp39 expression or inhibiting the
 XX gp39/CD40 interaction comprising administering an antibody specific for
 XX gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-
 XX cell activation; (2) an antibody which antagonises B-cell differentiation
 XX and antibody production, and is non-agonistic of T-cell activation; (3)
 XX a DNA sequence which encodes an antibody defined above; (4) an expression
 XX humoral and/or cellular immune responses against cells or vectors
 XX administered during cell or gene therapy comprising further administering
 XX prior, during or after gene therapy, an antibody defined above; and (6)
 XX an improved method of treatment which involves the transplantation of
 XX cells, tissues or organs of the same or different species into a subject,
 XX where the improvement comprises administering an antibody defined above
 XX prior, during or after transplantation, to suppress immune responses
 XX against the transplanted cell, tissue or organ, or to suppress immune
 XX responses elicited by the transplanted cell, tissue or organ against the
 XX host. The antibody is useful for preventing graft rejection, and for

CC treating autoimmune diseases, e.g., rheumatoid arthritis, multiple
 CC sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions,
 CC diabetes mellitus, or systemic lupus erythematosus, as well as non-
 CC autoimmune diseases such as graft-versus-host disease (many other
 CC diseases and conditions are given in the specification). The antibodies
 CC are also useful in gene or cellular therapy, and to inhibit humoral and
 CC cellular immune responses against viral vectors. The present sequence is
 CC a framework region (FR) fragment of a human anti-gp39 antibody used to
 CC determine which amino acids should be humanised in a mouse anti-gp39
 CC molecule
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 124; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 6.9e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 DB 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 RESULT 4
 ABG98301
 ID ABG98301 standard; peptide; 30 AA.
 XX
 AC ABG98301;
 DT 08-JAN-2003 (first entry)
 XX
 DE Human antibody 3d75d germline kappa chain variable region FRI.
 XX
 KW Antibody; variable region; light chain; heavy chain; VH; gp39; CD40;
 KW T-cell activation; B-cell differentiation; framework region;
 KW cellular immune response; gene therapy; graft rejection; human; FR;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
 KW asthma; multiple sclerosis; allergy; diabetes mellitus;
 KW systemic lupus erythematosus; graft-versus-host disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200194586-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 06-JUN-2001; 2001WO-US018098.
 XX
 PR 06-JUN-2000; 2000US-0209584P.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Pan LZ, Hanna N, Rastetter WH, Klotzter WS;
 XX
 XX WPI; 2002-188261/24.
 XX
 XX New antibodies binding to an epitope on gp39, useful for preventing graft
 XX rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or
 XX multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
 XX disease).
 XX
 XX Disclosure; Page 47; 130pp; English.
 XX
 XX The invention relates to an antibody which binds to an epitope on gp39,
 CC is new, where the epitope is distinct from the epitope bound by IDEC-131,
 CC and the antibody has a non-agonistic effect on T-cell activation and
 CC inhibits gp39/CD40 interaction. Also included are: (1) an improved method
 CC of treating a disease by modulating gp39 expression or inhibiting the
 CC gp39/CD40 interaction comprising administering an antibody specific for
 CC gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-
 CC cell activation; (2) an antibody which antagonises B-cell differentiation
 CC and antibody production, and is non-agonistic of T-cell activation; (3)
 CC a DNA sequence which encodes an antibody defined above; (4) an expression
 CC vector, which contains a DNA sequence of (3); (5) a method of suppressing

CC humoral and/or cellular immune responses against cells or vectors
 CC administered during cell or gene therapy comprising further administering
 CC prior, during or after gene therapy, an antibody defined above; and (6)
 CC an improved method of treatment which involves the transplantation of
 CC cells, tissues or organs of the same or different species into a subject,
 CC where the improvement comprises administering an antibody defined above
 CC against the transplanted cell, tissue or organ, or to suppress immune
 CC responses elicited by the transplanted cell, tissue or organ, and for
 CC host. The antibody is useful for preventing graft rejection, and for
 CC treating autoimmune diseases, e.g., rheumatoid arthritis, multiple
 CC sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions,
 CC diabetes mellitus, or systemic lupus erythematosus, as well as non-
 CC autoimmune diseases such as graft-versus-host disease (many other
 CC diseases and conditions are given in the specification). The antibodies
 CC are also useful in gene or cellular therapy, and to inhibit humoral and
 CC cellular immune responses against viral vectors. The present sequence is
 CC a framework region (FR) fragment of a human anti-gp39 antibody used to
 CC determine which amino acids should be humanised in a mouse anti-gp39
 CC molecule
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 124; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 6.9e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 DB 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
 RESULT 5
 AAU70466
 ID AAU70466 standard; peptide; 30 AA.
 XX
 AC AAU70466;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human heavy chain immunoglobulin framework region 1 #2.
 XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IGBP;
 KW transgenic plant; immunoglobulin binding protein array; IGM; IGA;
 KW IGD; IGE; IGY; IGM; kappa; lambda; CHBP.
 XX
 OS Homo sapiens.
 XX
 XX WO200183806-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014349.
 XX
 PR 02-MAY-2000; 2000US-00563222.
 XX
 PA (EPIC-) EPICYTE PHARM INC.
 XX
 PI Hiatt AC, Hein MB;
 XX
 XX WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 XX transforming the cells with different polynucleotides encoding binding
 XX protein polypeptides specific to ligand, selecting plant cells for
 XX preparing array.
 XX
 XX Disclosure; Fig 1B; 129pp; English.
 XX
 XX The invention relates to transforming a population of cells (e.g. plant
 XX cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides

CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transfected plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IGBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 XX Sequence 30 AA;

Query Match 100.0%; Score 124; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 6.9e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 6

ADY31417
 ID ADY31417 standard; peptide; 30 AA.

AC ADY31417;

DT 05-MAY-2005 (first entry)

DE Human antibody heavy chain framework peptide - SEQ ID 249.

XX DNA library; humanized antibody; antibody engineering; heavy chain.

KW Homo sapiens.

OS US2005042664-A1.

PN 24-FEB-2005.

PP 20-AUG-2004; 2004US-00923068.

XX 22-AUG-2003; 2003US-0497213P.

PR 13-OCT-2003; 2003US-0510741P.

XX (MEDI-) MEDIMUNE INC.

PI Wu H, Dall-Acqua W, Damschroder M;

XX WPI; 2005-180802/19.

DR New library of nucleic acid sequences comprises nucleotide sequences
 PT encoding humanized heavy chain variable regions and humanized light chain
 PT variable regions, useful for producing humanized antibodies.

XX Disclosure; SEQ ID NO 249; 179pp; English.

XX The invention comprises a library of nucleotide sequences encoding
 CC humanized antibody heavy chain variable regions and humanized antibody
 CC light chain variable regions. The library of the invention is useful for
 CC producing humanized antibodies, or for re-engineering or reshaping an
 CC antibody from a first species for use in a second species. The present
 CC amino acid sequence represents a human germline heavy chain framework
 CC peptide.

XX Sequence 30 AA;

Query Match 100.0%; Score 124; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 6.9e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 7

AEA21493
 ID AEA21493 standard; peptide; 30 AA.

XX AEA21493;

DT 28-JUL-2005 (first entry)

XX Human anti-SLPI antibody-related peptide SeqID57.

XX antibody; cytostatic; immunotherapy; cancer.

XX Homo sapiens.

XX WO2005047328-A2.

XX 26-MAY-2005.

XX 08-NOV-2004; 2004WO-US038634.

XX 07-NOV-2003; 2003US-0518275P.

XX (CURA-) CURAGEN CORP.

XX Gulshan A, Chui D, Larochelle WJ, Gallo ML, Zhong H;

XX WPI; 2005-367001/37.

XX New isolated human antibody that specifically binds to secretory
 PT leukocyte protease inhibitor (SLPI), useful for treating and preventing
 PT cancer.

XX Example 8; SEQ ID NO 57; 97pp; English.

XX This invention relates to a novel isolated human antibody that
 CC specifically binds to secretory leukocyte protease inhibitor (SLPI). The
 CC invention may be useful for the development of compounds with a
 CC cytostatic activity or for immunotherapy. The antibody, composition and
 CC methods are useful for treating and preventing cancer. The antibodies are
 CC useful for detecting the presence of SLPI in biological samples. The
 CC present sequence is that of a peptide which was used during the
 CC development of the novel antibody of the invention.

XX Sequence 30 AA;

Query Match 100.0%; Score 124; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 6.9e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 8

AEA21457
 ID AEA21457 standard; peptide; 30 AA.

XX AEA21457;

DT 28-JUL-2005 (first entry)

XX Human anti-SLPI antibody-related peptide SeqID21.

XX antibody; cytostatic; immunotherapy; cancer.

XX Homo sapiens.

[illegible]

CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
 CC consensus protein of the invention.

XX Sequence 95 AA;

Query Match 100.0%; Score 124; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 |||||
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 11

ADF09871
 ID ADF09871 standard; protein; 95 AA.

XX
 AC ADF09871;

DT 12-FEB-2004 (first entry)

DE Anti-MUC18 monoclonal antibody-related consensus protein #9.

XX cell proliferation inhibition; MUC18 tumour antigen;
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 KW carcinoma; cancer; malignancy; consensus.

XX Synthetic.

XX WO2003057837-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-598367/56.

XX Inhibiting cell proliferation associated with expression of MUC18 tumor
 PT antigen, involves incubating and inhibiting cell by administering anti-
 PT MUC18 monoclonal antibody.

XX Example 2; SEQ ID NO 58; 83pp; English.

XX The invention comprises a method for inhibiting cell proliferation
 CC associated with expression of MUC18 tumour antigen. The method involves
 CC administering anti-MUC18 monoclonal antibody. The method of the invention
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
 CC proliferation associated with the expression of MUC18 tumour antigen, the
 CC method is preferably useful for inhibiting tumour metastasis. The method
 CC is useful for inhibiting cell proliferation in patients with tumours,
 CC carcinomas, cancer and other malignancies. The present amino acid
 CC sequence is a consensus sequence from an alignment between an MUC18
 CC tumour antigen-specific monoclonal antibody of the invention and a
 CC related protein.

XX Sequence 95 AA;

Query Match 100.0%; Score 124; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 |||||
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 12

ADC99849
 ID ADC99849 standard; protein; 98 AA.

XX
 AC ADC99849;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody-related consensus protein SEQ ID 78.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer.

XX Unidentified.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

XX Example 2; SEQ ID NO 78; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 antibody-related
 CC consensus protein of the invention derived from analysis of germline gene
 CC region proteins and anti-human MUC18 monoclonal antibody sequences.

XX Sequence 98 AA;

Query Match 100.0%; Score 124; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 |||||
 Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 13

ADD05453
 ID ADD05453 standard; protein; 98 AA.

XX
 AC ADD05453;

DT 01-JAN-2004 (first entry)

XX DE Anti-MUC18 antibody heavy chain variable region V4-31 consensus protein.
 XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
 XX OS Unidentified.
 XX FN WO2003057006-A2.
 XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041582.
 XX PR 28-DEC-2001; 2001US-0346460P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas J, Bar-Eli M;
 XX DR WPI; 2003-577496/54.
 XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.
 XX PS Disclosure; SEQ ID NO 78; 87pp; English.
 XX CC The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC amino acids given in any one of 10 fully defined sequences of 117-123
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,
 CC consensus protein of the invention.
 XX CC
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 124; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0;
 QY 1 QVQLQESGPGLVKPSQTLISLTCTVS 25
 Db 1 QVQLQESGPGLVKPSQTLISLTCTVS 25
 RESULT 14
 ADF09891
 ID ADF09891 standard; protein; 98 AA.
 XX AC ADF09891;
 XX DT 12-FEB-2004 (first entry)
 XX DE Anti-MUC18 monoclonal antibody-related consensus protein #19.
 XX KW cell proliferation inhibition; MUC18 tumour antigen;
 XX KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 XX KW carcinoma; cancer; malignancy; consensus.
 XX OS Synthetic.
 XX FN WO2003057837-A2.

XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041580.
 XX PR 28-DEC-2001; 2001US-0346414P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas J;
 XX DR WPI; 2003-598367/56.
 XX PT Inhibiting cell proliferation associated with expression of MUC18 tumor
 PT antigen, involves incubating and inhibiting cell by administering anti-
 PT MUC18 monoclonal antibody.
 XX PS Example 2; SEQ ID NO 78; 83pp; English.
 XX CC The invention comprises a method for inhibiting cell proliferation
 CC associated with expression of MUC18 tumour antigen. The method involves
 CC administering anti-MUC18 monoclonal antibody. The method of the invention
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
 CC proliferation associated with the expression of MUC18 tumour antigen, the
 CC method is preferably useful for inhibiting tumour metastasis. The method
 CC is useful for inhibiting cell proliferation in patients with tumours,
 CC carcinomas, cancer and other malignancies. The present amino acid
 CC sequence is a consensus sequence from an alignment between an MUC18
 CC tumour antigen-specific monoclonal antibody of the invention and a
 CC related protein.
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 124; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0;
 QY 1 QVQLQESGPGLVKPSQTLISLTCTVS 25
 Db 1 QVQLQESGPGLVKPSQTLISLTCTVS 25
 RESULT 15
 ASG78215
 ID ASG78215 standard; protein; 99 AA.
 XX AC ASG78215;
 XX DT 15-NOV-2002 (first entry)
 XX DE Human Fv molecule hypervariable region related peptide #90.
 XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; melanoma; acute myeloid leukaemia.
 XX OS Homo sapiens.
 XX FN WO200259264-A2.
 XX PD 01-AUG-2002.
 XX PF 31-DEC-2001; 2001WO-US049440.
 XX PR 29-DEC-2000; 2000US-00751181.
 XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX DR WPI; 2002-619166/66.
 XX XX

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS
XX Claim 13; Page 194-195; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 124; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
| | | | | | | | | | | | | | | | | | | | | |
DB 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

Search completed: April 25, 2006, 06:15:10
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 33.7264 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-2

Perfect score: 124

Sequence: 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

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Database : Issued Patents AA:*

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- 6: /cgm2_6/ptodata/1/iaa/backfiles1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	124	100.0	30	2 US-09-563-222C-137	Sequence 137, App
2	124	100.0	87	2 US-08-554-840-19	Sequence 19, Appl
3	124	100.0	87	2 US-08-554-840-20	Sequence 20, Appl
4	124	100.0	87	2 US-08-525-333-19	Sequence 19, Appl
5	124	100.0	87	2 US-08-925-339-20	Sequence 20, Appl
6	124	100.0	87	2 US-09-332-595-19	Sequence 19, Appl
7	124	100.0	87	2 US-09-332-595-20	Sequence 20, Appl
8	124	100.0	95	2 US-10-330-613A-58	Sequence 58, Appl
9	124	100.0	98	2 US-10-330-613A-78	Sequence 78, Appl
10	124	100.0	99	2 US-10-194-975-36	Sequence 36, Appl
11	124	100.0	99	2 US-10-194-975-38	Sequence 38, Appl
12	124	100.0	99	2 US-10-194-975-39	Sequence 39, Appl
13	124	100.0	99	2 US-10-330-613A-45	Sequence 45, Appl
14	124	100.0	99	2 US-10-330-613A-46	Sequence 46, Appl
15	124	100.0	99	2 US-10-330-613A-57	Sequence 57, Appl
16	124	100.0	99	2 US-10-330-613A-65	Sequence 65, Appl
17	124	100.0	99	2 US-10-330-613A-77	Sequence 77, Appl
18	124	100.0	99	2 US-10-330-613A-77	Sequence 77, Appl
19	124	100.0	117	2 US-10-330-613A-5	Sequence 5, Appl
20	124	100.0	117	2 US-10-330-613A-13	Sequence 13, Appl
21	124	100.0	118	2 US-08-545-809A-116	Sequence 116, App
22	124	100.0	118	2 US-09-515-697-116	Sequence 116, App
23	124	100.0	119	1 US-08-360-125-5	Sequence 5, Appl
24	124	100.0	119	1 US-08-450-578-5	Sequence 5, Appl
25	124	100.0	119	1 US-09-017-628-5	Sequence 5, Appl
26	124	100.0	119	1 US-09-014-880-5	Sequence 5, Appl
27	124	100.0	119	2 US-08-450-363-5	Sequence 5, Appl

28	124	100.0	119	2	US-09-467-903-5	Sequence 5, Appl
29	124	100.0	119	2	US-10-330-613A-25	Sequence 25, Appl
30	124	100.0	136	2	US-09-471-276-838	Sequence 838, App
31	121	97.6	30	1	US-08-137-117D-128	Sequence 128, App
32	121	97.6	30	1	US-08-137-117D-135	Sequence 135, App
33	121	97.6	30	1	US-08-436-717-128	Sequence 128, App
34	121	97.6	30	1	US-08-436-717-135	Sequence 135, App
35	121	97.6	76	2	US-08-554-840-21	Sequence 21, Appl
36	121	97.6	76	2	US-08-925-339-21	Sequence 21, Appl
37	121	97.6	76	2	US-09-332-595-21	Sequence 16, Appl
38	121	97.6	87	2	US-08-554-840-16	Sequence 16, Appl
39	121	97.6	87	2	US-09-332-595-16	Sequence 16, Appl
40	121	97.6	87	2	US-10-330-613A-70	Sequence 70, Appl
41	121	97.6	96	2	US-10-330-613A-42	Sequence 42, Appl
42	121	97.6	96	2	US-10-330-613A-50	Sequence 50, Appl
43	121	97.6	97	2	US-10-194-975-42	Sequence 42, Appl
44	121	97.6	97	2	US-10-194-975-51	Sequence 51, Appl
45	121	97.6	97	2	US-10-194-975-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1

US-09-563-222C-137
; Sequence 137, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 137
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-137

Query Match 100.0%; Score 124; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
DB 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 2

US-08-554-840-19
; Sequence 19, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabill
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia

;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/554,840
;; FILING DATE: 07-NOV-1995
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-127
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 87 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-554-840-19

Query Match 100.0%; Score 124; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 3
US-08-554-840-20
;; Sequence 20, Application US/08554840
;; Patent No. 6001358
;; GENERAL INFORMATION:
;; APPLICANT: BLACK, Amelia
;; APPLICANT: HANNA, Nabil
;; APPLICANT: PADLAN, Eduardo A.
;; APPLICANT: NEWMAN, Roland A.
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9P39,
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/554,840
;; FILING DATE: 07-NOV-1995
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-127
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 87 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-554-840-20

Query Match 100.0%; Score 124; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 4
US-08-925-339-19
;; Sequence 19, Application US/08925339
;; Patent No. 6440418
;; GENERAL INFORMATION:
;; APPLICANT: BLACK, Amelia
;; APPLICANT: HANNA, Nabil
;; APPLICANT: PADLAN, Eduardo A.
;; APPLICANT: NEWMAN, Roland A.
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9P39,
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/925,339
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/554,840
;; FILING DATE: 07-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-127
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 87 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-925-339-19

Query Match 100.0%; Score 124; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 5

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US-08-925-339-20
; Sequence 20, Application US/08925339
; Patent No. 6440418
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-8620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-925-339-20

Query Match 100.0%; Score 124; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 1 QVQLQESGGPGLVKPSQTLSLTCTVS 25

RESULT 6
US-09-332-595-19
; Sequence 19, Application US/09332595
; Patent No. 6506383
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-332-595-20

Query Match 100.0%; Score 124; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 8
US-10-330-613A-58
; Sequence 58, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-58

Query Match 100.0%; Score 124; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 9
US-10-330-613A-78
; Sequence 78, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-78

Query Match 100.0%; Score 124; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 10
US-10-194-975-36
; Sequence 36, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-36

Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 11
US-10-194-975-38
; Sequence 38, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-38

Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 12
US-10-194-975-39
; Sequence 39, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; 
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; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-39

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Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

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RESULT 13
US-10-330-613A-45
; Sequence 45, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-45

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Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

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RESULT 14
US-10-330-613A-46
; Sequence 46, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-46

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Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

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RESULT 15
US-10-330-613A-57
; Sequence 57, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-57

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Query Match 100.0%; Score 124; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

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Search completed: April 25, 2006, 06:28:41
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	Score	Match	Length			
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2	124	100.0	99	2	S26803	Ig heavy chain V r
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4	124	100.0	137	2	S31585	Ig heavy chain V r
5	121	97.6	97	2	S26804	Ig heavy chain V r
6	121	97.6	97	2	S26906	Ig heavy chain V r
7	121	97.6	97	2	PH0876	Ig heavy chain V r
8	121	97.6	98	2	S12421	Ig heavy chain V r
9	121	97.6	99	2	S26807	Ig heavy chain V r
10	121	97.6	105	2	S44125	Ig lambda chain V
11	121	97.6	115	2	S57464	Ig heavy chain V-J
12	121	97.6	116	2	B26340	Ig heavy chain pre
13	121	97.6	116	2	S18557	Ig heavy chain V r
14	121	97.6	118	2	S20780	Ig heavy chain V r
15	121	97.6	118	2	A26340	Ig heavy chain pre
16	121	97.6	121	2	S44113	Ig heavy chain V r
17	121	97.6	123	2	S30530	Ig heavy chain - h
18	121	97.6	128	2	S31514	Ig heavy chain V r
19	121	97.6	130	2	S31690	Ig heavy chain V r
20	121	97.6	130	2	S31673	Ig heavy chain V r
21	121	97.6	137	2	S31676	Ig heavy chain V r
22	121	97.6	137	2	S31696	Ig heavy chain V r
23	121	97.6	139	2	S31586	Ig heavy chain V r
24	121	97.6	140	2	S37882	Ig variable region
25	121	97.6	140	2	A24770	hypothetical hybrid
26	121	97.6	155	2	S31512	Ig heavy chain - h
27	121	97.6	155	2	S31511	Ig heavy chain - h
28	119	96.0	97	2	S12416	Ig heavy chain V r
29	119	96.0	99	2	S26802	Ig heavy chain V r

A:Residue: 1-99 <WEN>

A;Residues: 1-99 <WEN>

Best Local Similarity 96.0%; Pred.No. 2e-11; Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
| | | | | : | | | | | | | | | |
DB 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 10
S44125
Ig lambda chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44125
R: Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.;
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of v
A:Reference number: S44105
A:Accession: S44125
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <RAW>
C:Cross-references: UNIPARC:UPI00011662A; EMBL:Z31383; NID:g472978; PIDN:CAA83
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-97/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 105;
Best Local Similarity 96.0%; Pred.No. 2.1e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
| | | | | : | | | | | | | | | |
DB 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 11
S57464
Ig heavy chain V-J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S57464
R: Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A:Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from moto
A:Reference number: S57408
A:Accession: S57464
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <PAT>
A:Cross-references: UNIPARC:UPI0001137AD; EMBL:X87897; NID:g871273; PIDN:CAA6
C:Genetics:
A: Introns: 100/2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:15-99/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 115;
Best Local Similarity 96.0%; Pred.No. 2.3e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
| | | | | : | | | | | | | | | |
DB 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 12
B26340
Ig heavy chain precursor V-II region (71-4) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1998 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: B26340
R: Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo
J. Mol. Biol. 190, 529-541, 1986

A;Title: Organization and evolution of variable region genes of the human immunoglobulin
A;Reference number: A26340; MUID:87061007; PMID:3097326
A;Accession: B26340
A;Molecule type: DNA
A;Residues: 1-116 <KOD>
A;Cross-references: UNIPARC:UPI0000115D70; GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 116;
Best Local Similarity 96.0%; Pred.No. 2.3e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKPESQTLSTLTCTVS 25
Db 20 QVQLQESGPGGLVKPESQTLSTLTCTVS 44

RESULT 13
S18557
Ig heavy chain V region precursor (VIV-4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18557
R;Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18557
A;Molecule type: DNA
A;Residues: 1-116 <SHA>
A;Cross-references: UNIPARC:UPI0000115FF0; EMBL:X62112; NID:g37853; PIDN:CAA44022.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-116/Product: Ig heavy chain V region (VIV-4) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 116;
Best Local Similarity 96.0%; Pred.No. 2.3e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKPESQTLSTLTCTVS 25
Db 20 QVQLQESGPGGLVKPESQTLSTLTCTVS 44

RESULT 14
S20780
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain Iga and IgG repertoire.
A;Reference number: S20764
A;Accession: S20780
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <MOR>
A;Cross-references: UNIPARC:UPI00001163F6; EMBL:Z11598; NID:g33893; PIDN:CAA78015.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 118;
Best Local Similarity 96.0%; Pred.No. 2.4e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKPESQTLSTLTCTVS 25
Db 1 QVQLQESGPGGLVKPESQTLSTLTCTVS 25

RESULT 15

A26340
Ig heavy chain precursor V-II region (71-2) - human
N;Alternate names: Ig heavy chain V region (DP-66)
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1998 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A26340; S26901
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin
A;Reference number: A26340; MUID:87061007; PMID:3097326
A;Accession: A26340
A;Molecule type: DNA
A;Residues: 1-118 <KOD>
A;Cross-references: UNIPARC:UPI000011B546; GB:M29811; NID:g185597; PIDN:AAC99493.1; PID:
A;Note: the authors translated the codon GAG for residue 25 as Gln
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26985; MUID:93021117; PMID:1404388
A;Accession: S26901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 20-118 <TOM>
A;Cross-references: UNIPARC:UPI000011641A; EMBL:Z12366; NID:g32950; PIDN:CAA78236.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-118/Product: Ig heavy chain V-II region 71-2 #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 121; DB 2; Length 118;
Best Local Similarity 96.0%; Pred.No. 2.4e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKPESQTLSTLTCTVS 25
Db 20 QVQLQESGPGGLVKPESQTLSTLTCTVS 44

Search completed: April 25, 2006, 06:26:12
Job time : 21.2264 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 133,491 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-2

Perfect score: 124

Sequence: 1 QVQLQSGPLGKLPSTLSLTCTVS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	100.0	476	Q6GMX1_HUMAN	Q6gm1 homo sapien
2	124	100.0	478	Q72379_HUMAN	Q72379 homo sapien
3	121	97.6	119	Q9UL73_HUMAN	Q9ul73 homo sapien
4	121	97.6	139	Q86SX2_HUMAN	Q86sx2 homo sapien
5	121	97.6	465	Q6GMX6_HUMAN	Q6gm6 homo sapien
6	121	97.6	477	Q6GMX7_HUMAN	Q6gm7 homo sapien
7	121	97.6	620	Q9EY0_HUMAN	Q9ey0 homo sapien
8	118	95.2	130	Q8IZD7_HUMAN	Q8izd7 homo sapien
9	118	95.2	492	Q72374_HUMAN	Q72374 homo sapien
10	116	93.5	477	Q510J1_RAT	Q510j1 rattus norv
11	115	92.7	117	HV2G_HUMAN	P01825 homo sapien
12	115	92.7	122	Q9UL75_HUMAN	Q9ul75 homo sapien
13	114	91.9	150	Q95973_HUMAN	Q95973 homo sapien
14	113	91.1	469	Q5M839_RAT	Q5m839 rattus norv
15	113	91.1	591	Q510L9_RAT	Q510l9 rattus norv
16	112	90.3	478	Q6NYH3_HUMAN	Q6nyh3 homo sapien
17	112	90.3	576	Q6P418_HUMAN	Q6p418 homo sapien
18	110	88.7	496	Q96KX8_HUMAN	Q96kx8 rattus norv
19	110	88.7	590	Q569B8_RAT	Q569b8 rattus norv
20	110	88.7	615	Q569B6_RAT	Q569b6 rattus norv
21	108	87.1	98	Q53VQ0_MOUSE	Q53vq0 mus musculus
22	108	87.1	98	Q53VQ4_MOUSE	Q53vq4 mus musculus
23	108	87.1	98	Q53VQ8_MOUSE	Q53vq8 mus musculus
24	108	87.1	98	Q53VR2_MOUSE	Q53vr2 mus musculus
25	108	87.1	113	HV47_MOUSE	P01823 mus musculus
26	108	87.1	115	HV44_MOUSE	P01820 mus musculus
27	108	87.1	115	Q53VQ1_MOUSE	Q53vq1 mus musculus
28	108	87.1	116	HV60_MOUSE	P18531 mus musculus
29	108	87.1	119	Q53VQ5_MOUSE	Q53vq5 mus musculus
30	108	87.1	119	Q53VQ9_MOUSE	Q53vq9 mus musculus
31	108	87.1	119	Q53VR3_MOUSE	Q53vr3 mus musculus

Q99NG4 mus musculus
P01824 homo sapien
Q61BQ5 mus musculus
P01822 mus musculus
P01819 mus musculus
Q65Z11 mus musculus
Q99M22 mus musculus
P01821 mus musculus
P18533 mus musculus
Q8tc63 homo sapien
Q5m842 rattus norv
P18532 mus musculus
Q5U413 mus musculus
Q53VR6 mus musculus

121 2 Q99NG4_MOUSE
129 1 HV2P_HUMAN
136 2 Q61BQ5_MOUSE
137 1 HV46_MOUSE
144 1 HV43_MOUSE
262 2 Q65Z11_MOUSE
479 2 Q99M22_MOUSE
116 1 HV45_MOUSE
117 1 HV62_MOUSE
473 2 Q8TC63_HUMAN
458 2 Q5M842_RAT
116 1 HV61_MOUSE
483 2 Q5U413_MOUSE
98 2 Q53VR6_MOUSE

ALIGNMENTS

RESULT 1

Q6GMX1_HUMAN

ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.

AC Q6GMX1; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

EN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Splice;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.B.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Splice;

RC Strausberg R.L.

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073773; AAH73773.1; -, mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig.c1.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 100.0%; Score 124; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKKPSQTLISLTCTVS 25
Db 20 QVQLQESGPGGLVKKPSQTLISLTCTVS 44

RESULT 2
Q72379_HUMAN
ID Q72379 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX38066; CAD97996.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SNR; Q72379; 248-456.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IG_V.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCEB541F3217CA1 CRC64;

Query Match 100.0%; Score 124; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKKPSQTLISLTCTVS 25
Db 19 QVQLQESGPGGLVKKPSQTLISLTCTVS 43

RESULT 3
Q9UL73_HUMAN
ID Q9UL73 HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2511001;
RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
RT "The smaller human VH gene families display remarkably little
polymorphism.";
RL EMBO J. 8:3741-3748(1989).
DR EMBL; AF035041; AAD56277.1; -; mRNA.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR SNR; Q9UL73; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 97.6%; Score 121; DB 2; Length 119;
Best Local Similarity 96.0%; Pred. No. 1.1e-10;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGGLVKKPSQTLISLTCTVS 25
Db 1 QVQLQESGPGGLVKKPSQTLISLTCTVS 25

RESULT 4
Q86SX2_HUMAN
ID Q86SX2 HUMAN PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSODL004YWL9 of B cells (Ramos cell line) of
DE Homo sapiens (human) (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SNR; Q86SX2; 33-129.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
```

DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 97.6%; Score 121; DB 2; Length 139;
Best Local Similarity 96.0%; Pred. No. 1.2e-10;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLISLTCTVS 25
|||
DD 33 QVQLQESGPGLVKPSSETLSLTCTVS 57
|||

RESULT 5
Q6GMX6 HUMAN Q6GMX6 HUMAN PRT; 465 AA.
ID Q6GMX6 HUMAN PRELIMINARY;
AC Q6GMX6 AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD81386E CRC64;

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Db 20 QVQLQESGPGGLVKPSETLSLTCTVS 44
|||||
Query Match 97.6%; Score 121; DB 2; Length 620;
Best Local Similarity 96.0%; Pred. No. 6.3e-10;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
Q96EYO HUMAN
ID Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.
AC Q96EYO
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schein M.C., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Primary B-Cells;
RG NIH WGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1304154;
RA Neale G.A., Kitchingman G.R.;
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT chain enhancer region contain a non-translatable exon and are
RT extremely heterogeneous at the 5' end."
RL Nucleic Acids Res. 19:2427-2433(1991).
DR EMBL; BC011857; AAL1857.2; -, mRNA.
DR PIR; S15590; S15590.
DR HSP; P01820; IG7J.
DR SMR; Q96EYO; 27-251.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 95.28; Score 118; DB 2; Length 130;
Best Local Similarity 92.0%; Pred. No. 3.4e-10;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Q81ZD7 HUMAN
ID Q81ZD7 HUMAN PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -, mRNA.
DR HSP; P01820; IG7J.
DR SMR; Q81ZD7; 1-130.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 92.0%; Score 118; DB 2; Length 130;
Best Local Similarity 92.0%; Pred. No. 3.4e-10;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
Q7Z374 HUMAN
ID Q7Z374 HUMAN PRELIMINARY; PRT; 492 AA.
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -, mRNA.
DR HSP; P01820; IG7J.
DR SMR; Q7Z374; 262-470.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 95.2%; Score 118; DB 2; Length 492;
Best Local Similarity 92.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 32 QLQLQESGPGLVKPSQTLSTCTVS 56

RESULT 10
Q510J1 RAT PRELIMINARY; PRT; 477 AA.
ID Q510J1
AC Q510J1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igha protein.
GN Igha
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson K.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088269; AAH88269.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.CI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 477 AA; 52167 MW; 226460762898C6F0 CRC64;

Query Match 93.5%; Score 116; DB 2; Length 477;
Best Local Similarity 92.0%; Pred. No. 2.9e-09;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 20 QVQLKESGPGLVKPSQTLSTCTVS 44

RESULT 11
HV2G HUMAN STANDARD; PRT; 117 AA.
ID HV2G_HUMAN
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region NEMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77242302; PubMed=407927;
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT "Amino acid sequence of the VH region of a human myeloma
immunoglobulin (IgG New).";
RL Biochemistry 16:3412-3420 (1977).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF PAB FRAGMENT.
RX MEDLINE=78066916; PubMed=618887;
RA Saul F.A., Anzel L.M., Poljak R.J.;
RT "Preliminary refinement and structural analysis of the Fab fragment
from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597 (1978).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A90404; G1HUNM.
CC PDB; 7FAB; X-ray; H=2-117.
CC SMR; P01825; 2-117.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyridoxine carboxylic acid.
FT DOMAIN 1 111
FT MOD_RES 1 111
FT NON_TER 117 117
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 30 31
FT TURN 33 39
FT TURN 41 42
FT STRAND 46 51
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FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 92.7%; Score 115; DB 1; Length 117;
Best Local Similarity 88.0%; Pred. No. 9e-10;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
   ||||:|||||:|||||:|||||:
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 12
ID Q9UL75 HUMAN PRELIMINARY; PRT; 122 AA.
AC Q9UL75
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Barney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Schroeder H.W. Jr, Wang J.Y.;
RT "Preferential utilization of conserved immunoglobulin heavy chain
RT variable gene segments during human fetal life."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX Logtenberg T., Young F.M., Van Es J.H., Gmelig-Meyling F.H., Alt F.W.;
RT "Autoantibodies encoded by the most Jh-proximal human immunoglobulin
RT heavy chain variable region gene."
RL J. Exp. Med. 170:1347-1355(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
RT "The smaller human VH gene families display remarkably little
RT polymorphism."
RL EMBO J. 8:3741-3748(1989).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Bird J., Galili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia."
RL J. Exp. Med. 168:229-245(1988).
RN [6]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Oppiger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A."
RL J. Exp. Med. 178:331-336(1993).
DR EMBL; AF035039; AAD56275.1; -; mRNA.
DR PIR; D36006; D36006.
DR PIR; PH1674; PH1674.
DR PIR; PLO117; PLO117.
DR PIR; PLO160; PLO160.
DR PIR; PS0089; PS0089.
DR PIR; PS0090; PS0090.
DR PIR; PS0091; PS0091.
DR PIR; S12433; S12433.
DR PIR; S24700; S24700.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 92.7%; Score 115; DB 2; Length 122;
Best Local Similarity 88.0%; Pred. No. 9.4e-10;
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSQTLSTCTVS 25
   ||||:|||||:|||||:|||||:
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 13
ID Q95973 HUMAN PRELIMINARY; PRT; 150 AA.
AC Q95973
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Behcet's patient with arthritis."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1718404;
RA Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.E.,
RA Wilder R.L., Notkins A.L., Casali P.;
RT "Complete sequence of the genes encoding the VH and VL regions of low-
RT and high-affinity monoclonal IGM and IgA1 rheumatoid factors produced
RT by CD5+ B cells from a rheumatoid arthritis patient."
RL Int. Immunol. 3:865-875(1991).
DR EMBL; AF103795; AAC79084.1; -; mRNA.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR SMR; O95973; 20-147.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.

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FT SIGNAL 1 19 Potential.
 FT CHAIN 20 >150 VH4 heavy chain variable region.
 FT NON TER 150
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 91.9%; Score 114; DB 2; Length 150;
 Best Local Similarity 88.0%; Pred. No. 1.7e-09;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 Db 20 QQLQESGPGLVKPSQTLSTCTVS 44

RESULT 14
 QSM839 RAT PRELIMINARY; PRT; 469 AA.

AC QSM839
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Igh-1a predicted protein.
 GN Name=Igh-1a predicted;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=2398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Director MGC Project;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC088254; AAH8254.1; -; mRNA.
 DR GO; GO:000823; P:antigen binding; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.C1.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
 SQ SEQUENCE 469 AA; 51403 MW; 030A2C3C66228F16 CRC64;

Query Match 91.1%; Score 113; DB 2; Length 469;
 Best Local Similarity 88.0%; Pred. No. 1.1e-08;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 88.0%; Pred. No. 8.3e-09;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
 Db 20 QVQLQESGPGLVKPSQTLSTCTVS 44

RESULT 15
 Q5IOL9 RAT PRELIMINARY; PRT; 591 AA.

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 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE LOC366747 protein (Fragment).
 GN Name=LOC366747;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA NIH MGC Project;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC088184; AAH88184.1; -; mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.C1.
 DR InterPro; IPR003598; IG.C2.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.V.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 4.
 DR SMART; SM00408; IGV; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
 FT NON TER 1
 SQ SEQUENCE 591 AA; 64940 MW; 207CFE500D2C2A97 CRC64;

Query Match 91.1%; Score 113; DB 2; Length 591;
 Best Local Similarity 88.0%; Pred. No. 1.1e-08;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25

D**b** 21 EVQLKESGGPGLVQPSQITLSLTCTVS 45
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Search completed: April 25, 2006, 06:24:43
Job time : 134.491 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:58:17 ; Search time 108.962 Seconds
(without alignments)
95.866 Million cell updates/sec

Title: US-10-764-428-2

Perfect score: 124
Sequence: 1 QVQLQESGFLVKPSQTLSTCTVS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main: *
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep: *
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep: *
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep: *
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep: *
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	100.0	25	US-10-764-428-2	Sequence 2, Appl
2	124	100.0	25	US-10-923-068-381	Sequence 381, App
3	124	100.0	30	US-09-874-141-28	Sequence 28, Appl
4	124	100.0	30	US-09-874-141-29	Sequence 29, Appl
5	124	100.0	30	US-09-563-222-146	Sequence 146, App
6	124	100.0	30	US-10-783-950-137	Sequence 137, App
7	124	100.0	30	US-10-923-068-249	Sequence 249, App
8	124	100.0	30	US-10-984-960A-21	Sequence 21, Appl
9	124	100.0	30	US-10-984-960A-57	Sequence 57, Appl
10	124	100.0	87	US-10-171-681-19	Sequence 19, Appl
11	124	100.0	87	US-10-171-681-20	Sequence 20, Appl
12	124	100.0	87	US-10-171-680-19	Sequence 19, Appl
13	124	100.0	87	US-10-171-680-20	Sequence 20, Appl
14	124	100.0	99	US-10-194-975-36	Sequence 36, Appl
15	124	100.0	99	US-10-194-975-38	Sequence 38, Appl
16	124	100.0	99	US-10-194-975-39	Sequence 39, Appl
17	124	100.0	99	US-10-308-817-79	Sequence 79, Appl
18	124	100.0	99	US-10-308-817-81	Sequence 81, Appl
19	124	100.0	99	US-10-308-817-82	Sequence 82, Appl
20	124	100.0	99	US-10-032-037B-90	Sequence 90, Appl
21	124	100.0	99	US-10-029-988B-90	Sequence 90, Appl
22	124	100.0	99	US-10-032-423A-90	Sequence 90, Appl
23	124	100.0	99	US-10-309-762-7	Sequence 7, Appl
24	124	100.0	99	US-10-453-698-79	Sequence 79, Appl
25	124	100.0	99	US-10-453-698-81	Sequence 81, Appl
26	124	100.0	99	US-10-453-698-82	Sequence 82, Appl
27	124	100.0	99	US-10-029-926B-90	Sequence 90, Appl

28	124	100.0	99	4	US-10-379-392-45	Sequence 45, Appl
29	124	100.0	99	4	US-10-379-392-46	Sequence 46, Appl
30	124	100.0	99	5	US-10-984-960A-82	Sequence 82, Appl
31	124	100.0	107	3	US-09-864-761-47367	Sequence 47367, A
32	124	100.0	110	4	US-10-309-762-74	Sequence 74, Appl
33	124	100.0	110	5	US-10-727-155-272	Sequence 272, App
34	124	100.0	113	5	US-10-474-345-1	Sequence 1, Appl
35	124	100.0	117	4	US-10-330-613-5	Sequence 5, Appl
36	124	100.0	117	4	US-10-330-613-13	Sequence 13, Appl
37	124	100.0	117	4	US-10-330-530-5	Sequence 5, Appl
38	124	100.0	117	4	US-10-330-530-13	Sequence 13, Appl
39	124	100.0	117	4	US-10-660-357-5	Sequence 5, Appl
40	124	100.0	117	4	US-10-660-357-13	Sequence 13, Appl
41	124	100.0	117	5	US-10-735-916A-72	Sequence 72, Appl
42	124	100.0	118	4	US-10-078-757B-50	Sequence 50, Appl
43	124	100.0	118	4	US-10-309-762-138	Sequence 138, App
44	124	100.0	118	4	US-10-684-109-43	Sequence 43, Appl
45	124	100.0	119	4	US-10-330-613-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-764-428-2
; Sequence 2, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; FILE REFERENCE: 11669.120USUI
; CURRENT APPLICATION NUMBER: US/10/764,428
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FRI SGII
US-10-764-428-2

Query Match 100.0%; Score 124; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGFLVKPSQTLSTCTVS 25
DB 1 QVQLQESGFLVKPSQTLSTCTVS 25

RESULT 2
US-10-923-068-381
; Sequence 381, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE6000S
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 381
; LENGTH: 25
; TYPE: PRT

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/ ORGANISM: Homo sapiens
US-10-923-068-381

Query Match      100.0%; Score 124; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 3
US-09-874-141-28
; Sequence 28, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-28

Query Match      100.0%; Score 124; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 4
US-09-874-141-29
; Sequence 29, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-29

Query Match      100.0%; Score 124; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 5
US-09-563-222-146
; Sequence 146, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-146

Query Match      100.0%; Score 124; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 6
US-10-783-950-137
; Sequence 137, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-137

Query Match      100.0%; Score 124; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 7
US-10-923-068-249
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; Sequence 249, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-249

Query Match      100.0%; Score 124; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 8
US-10-984-960A-21
; Sequence 21, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: Larochele, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 21
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-21

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Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 9
US-10-984-960A-57
; Sequence 57, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ara, Gulshan
; APPLICANT: Larochele, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A

Query Match      100.0%; Score 124; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 57
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-984-960A-57

Query Match      100.0%; Score 124; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 10
US-10-171-681-19
; Sequence 19, Application US/10171681
; Publication No. US20030170233A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/171,681
; FILING DATE: 17-JUNE-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-171-681-19

Query Match      100.0%; Score 124; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 11
US-10-171-681-20
; Sequence 20, Application US/10171681
; Publication No. US20030170233A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/171,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/332,595
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-171-680-19
; Query Match 100.0%; Score 124; DB 4; Length 87;
; Best Local Similarity 100.0%; Pred. No. 3.5e-10;
; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 13
US-10-171-680-20
; Sequence 20, Application US/10171680
; Publication No. US20030175269A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

Qy 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTLTCTVS 25

RESULT 12
US-10-171-680-19
; Sequence 19, Application US/10171680
; Publication No. US20030175269A1
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/171,680
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/332,595
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-171-680-20

Query Match 100.0%; Score 124; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

Search completed: April 25, 2006, 07:08:49
Job time : 109.962 secs
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; APPLICATION NUMBER: US/10/171,680
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/332,595
; FILING DATE:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-171-680-20

Query Match 100.0%; Score 124; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25
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RESULT 14
US-10-194-975-36
; Sequence 36, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-36
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Query Match 100.0%; Score 124; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25
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RESULT 15
US-10-194-975-38
; Sequence 38, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-38
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Query Match 100.0%; Score 124; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds
(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-2

Perfect score: 124

Sequence: 1 QVQLQESGPGLVKPSQTLSTCTVS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /SIDSS/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	124	100.0	99	7	US-11-054-669-36
2	124	100.0	99	7	US-11-054-669-38
3	124	100.0	99	7	US-11-054-669-39
4	124	100.0	99	7	US-11-084-554-50
5	124	100.0	99	7	US-11-004-590-42
6	124	100.0	99	7	US-11-004-590-43
7	124	100.0	99	7	US-11-136-250-50
8	124	100.0	117	7	US-11-012-353-72
9	124	100.0	119	6	US-10-530-171-7
10	124	100.0	119	7	US-11-004-590-237
11	124	100.0	119	7	US-11-004-590-331
12	124	100.0	119	7	US-11-004-590-340
13	124	100.0	119	7	US-11-004-590-342
14	124	100.0	119	7	US-11-004-590-348
15	124	100.0	119	7	US-11-004-590-352
16	124	100.0	119	7	US-11-004-590-359
17	124	100.0	119	7	US-11-004-590-369
18	124	100.0	248	7	US-11-054-515-1960
19	124	100.0	248	7	US-11-266-444-1960
20	124	100.0	249	7	US-11-054-515-1962
21	124	100.0	249	7	US-11-266-444-1962
22	124	100.0	253	7	US-11-054-515-1619
23	124	100.0	253	7	US-11-266-444-1619
24	121	97.6	97	7	US-11-144-248-36
25	121	97.6	97	7	US-11-144-248-44

26	121	97.6	97	7	US-11-054-669-42	Sequence 42, Appl
27	121	97.6	97	7	US-11-054-669-51	Sequence 51, Appl
28	121	97.6	97	7	US-11-054-669-52	Sequence 52, Appl
29	121	97.6	97	7	US-11-084-554-53	Sequence 53, Appl
30	121	97.6	97	7	US-11-084-554-54	Sequence 54, Appl
31	121	97.6	97	7	US-11-144-222-36	Sequence 36, Appl
32	121	97.6	97	7	US-11-144-222-44	Sequence 44, Appl
33	121	97.6	97	7	US-11-004-590-46	Sequence 46, Appl
34	121	97.6	97	7	US-11-136-250-53	Sequence 53, Appl
35	121	97.6	97	7	US-11-136-250-54	Sequence 54, Appl
36	121	97.6	97	7	US-11-182-343-36	Sequence 36, Appl
37	121	97.6	97	7	US-11-182-343-44	Sequence 44, Appl
38	121	97.6	98	7	US-11-012-353-74	Sequence 74, Appl
39	121	97.6	99	7	US-11-054-669-43	Sequence 43, Appl
40	121	97.6	99	7	US-11-084-554-55	Sequence 55, Appl
41	121	97.6	99	7	US-11-004-590-47	Sequence 47, Appl
42	121	97.6	99	7	US-11-136-250-55	Sequence 55, Appl
43	121	97.6	108	6	US-10-939-866-6	Sequence 6, Appl
44	121	97.6	108	6	US-10-935-005B-36	Sequence 36, Appl
45	121	97.6	108	7	US-11-061-821-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-11-054-669-36
; Sequence 36, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 36
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-36

Query Match 100.0%; Score 124; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 2
US-11-054-669-38
; Sequence 38, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 38

Query Match 100.0%; Score 124; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 7

US-11-136-250-50
; Sequence 50, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: AGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; PRIOR FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-50

Query Match 100.0%; Score 124; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 8

US-11-012-353-72
; Sequence 72, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0206053
; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 72
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (59)
; OTHER INFORMATION: Variable amino acid
US-11-012-353-72

Query Match 100.0%; Score 124; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 9

US-10-530-171-7
; Sequence 7, Application US/10530171
; Publication No. US20060057147A1
; GENERAL INFORMATION:
; APPLICANT: HIRAKAWA, Youko
; APPLICANT: NIKI, Hisae
; APPLICANT: OIKE, Shinsuke
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: YOSHIYAMA, Yoshiko
; TITLE OF INVENTION: Antibody recognizing antigen
; FILE REFERENCE: 235054
; CURRENT APPLICATION NUMBER: US/10/530,171
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/JP2003/012732
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: JP 2002-291953
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-530-171-7

Query Match 100.0%; Score 124; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 10

US-11-004-590-237
; Sequence 237, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRAIN
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167

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; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 237
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-237

Query Match      100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 11
US-11-004-590-331
; Sequence 331, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 331
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-004-590-331

Query Match      100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 12
US-11-004-590-340
; Sequence 340, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
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; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 340
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-004-590-340

Query Match      100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 13
US-11-004-590-342
; Sequence 342, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 342
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-004-590-342

Query Match      100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

RESULT 14
US-11-004-590-348
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Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

Search completed: April 25, 2006, 07:10:02
Job time : 16.2044 secs

; Sequence 348, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 348
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-004-590-348

Query Match 100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVS 25
Db 1 QVQLQESGPGLVKPSQTLSTCTVS 25

RESULT 15
US-11-004-590-352
; Sequence 352, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 352
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-004-590-352

Query Match 100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 133.491 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-3

Perfect score: 123

Sequence: 1 EVQLVDSGGGLVQPGGSLRLSCAAS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	25	8	Adg92397 Human hul
2	123	100.0	25	8	Adg80586 Human hea
3	123	100.0	25	8	Adg90699 Anti-VSGF
4	123	100.0	25	9	Ady31507 Human ant
5	123	100.0	25	9	Ady31531 Human ant
6	123	100.0	25	9	Ady31534 Human ant
7	123	100.0	25	9	Ady31516 Human ant
8	123	100.0	25	9	Ady31483 Human ant
9	123	100.0	25	9	Ady31489 Human ant
10	123	100.0	25	9	Ady31540 Human ant
11	123	100.0	29	9	Adz07629 Mouse JA6
12	123	100.0	30	2	Aar87049 Human gro
13	123	100.0	30	5	Aae19691 Human gro
14	123	100.0	30	9	Adx27037 Human gro
15	123	100.0	30	9	Ady31384 Human ant
16	123	100.0	30	9	Ady31351 Human ant
17	123	100.0	30	9	Ady31399 Human ant
18	123	100.0	30	9	Ady31402 Human ant
19	123	100.0	30	9	Ady31408 Human ant
20	123	100.0	30	9	Ady31375 Human ant
21	123	100.0	30	9	Ady31357 Human ant
22	123	100.0	30	9	Aeb13673 Human ant
23	123	100.0	44	8	Adu87725 Human hea
24	123	100.0	58	9	Aec20858 Human var

25	123	100.0	60	9	ABC20855	Rec20855 Human var
26	123	100.0	72	4	AAm23728	AAm23728 Human EST
27	123	100.0	79	8	ABO54896	ABO54896 Human gen
28	123	100.0	87	8	ADK51391	ADK51391 Human ant
29	123	100.0	87	8	ADK51429	ADK51429 Human ant
30	123	100.0	87	8	ADU87732	ADU87732 Amino aci
31	123	100.0	93	6	ABO27274	ABO27274 Human hum
32	123	100.0	96	8	ADU04240	ADU04240 Human imm
33	123	100.0	97	3	ABAB40112	ABAB40112 Anti-hiL1
34	123	100.0	97	5	ABG78194	ABG78194 Human Fv
35	123	100.0	97	5	ABG78203	ABG78203 Human Fv
36	123	100.0	97	5	ABG91885	ABG91885 Human ant
37	123	100.0	97	5	ABG91894	ABG91894 Human ant
38	123	100.0	97	6	ABO27085	ABO27085 Human ger
39	123	100.0	97	6	ABO27098	ABO27098 Human ger
40	123	100.0	97	7	ADF100020	ADF100020 VEGF anti
41	123	100.0	97	7	ADF10038	ADF10038 VEGF anti
42	123	100.0	97	7	ADF09912	ADF09912 Antibody
43	123	100.0	97	7	ADF09930	ADF09930 Antibody
44	123	100.0	97	7	ADF10122	ADF10122 Antibody
45	123	100.0	97	7	ADF10140	ADF10140 Antibody

ALIGNMENTS

RESULT 1

ADQ92397
ID ADQ92397 standard; peptide; 25 AA.

XX AC ADQ92397;

DT 23-SEP-2004 (first entry)

XX Human hul FRH1 peptide.

DE
XX
KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;
KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;
KW neurodegenerative disease; malignancy; TNF-secreting tumour;
KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;
KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;
KW reperfusion injury; chronic obstructive pulmonary disease;
KW pulmonary fibrosis; hepatitis C infection; Kawasaki's disease;
KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;
KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;
KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;
KW hypokinetic movement disorder; drug-induced movement disorder;
KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;
KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;
KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;
KW human; heavy chain variable region; VH; FR; framework region.

XX Homo sapiens.

OS US2004131613-A1.

PD 08-JUL-2004.

XX 08-JAN-2003; 2003US-00338627.

XX 08-JAN-2003; 2003US-00338627.

XX (WATK/) WATKINS J D.

XX (VASS/) VASSEROT A P.

XX (MARQ/) MARQUIS D.

XX (HUSE/) HUSE W D.

PI Watkins JD, Vasserot AP, Marquis D, Huse WD;

XX WPI; 2004-524894/50.

DR N-PSDB; ADQ92401.

XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)

PT

PT binding molecule, useful for treating a TNF-alpha mediated disease such
 PT as sepsis, an autoimmune disease, rheumatoid arthritis, and
 PT neurodegenerative diseases.

XX Disclosure; SEQ ID NO 65; 60pp; English.

PS The present invention relates to tumour necrosis factor alpha (TNF-alpha)
 CC binding polypeptides and their encoding polynucleotides. The invention is
 CC useful for treating TNF-alpha mediated disease such as sepsis, an
 CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,
 CC neurodegenerative diseases, malignant pathologies involving TNF-secreting
 CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,
 CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,
 CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary
 CC fibrosis, hepatitis C infection, Kawasaki's pathology, Kefsum's disease,
 CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's
 CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic
 CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and
 CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced
 CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic
 CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes
 CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious
 CC diseases. The invention is also useful in antibody therapy. The present
 CC sequence is human hul framework sub-region of heavy chain variable (VH)
 CC region (FRH) peptide. This sequence is used in the invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 123; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVSGGGLVPGGSLRLSCAAS 25
 |||||
 Db 1 EVQLVSGGGLVPGGSLRLSCAAS 25

RESULT 2

ID AQ80586
 AD AQ80586 standard; peptide; 25 AA.

XX AQ80586;

XX 23-SEP-2004 (first entry)

XX Human heavy chain framework region FR1.

XX TNF-alpha binding; complementarity determining region; CDR; TNF-alpha;
 KW immunoassay; CDRH-3; CDRH-3; sepsis; autoimmune disease;
 KW rheumatoid arthritis; allergy; multiple sclerosis;
 KW systemic lupus erythematosus; scleroderma; diabetes mellitus; cachexia;
 KW parasitic disease; infectious disease; sarcoidosis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW disseminated intravascular coagulation; Parkinson's disease;
 KW Alzheimer's disease; Down's syndrome; psoriasis; ankylosing spondylitis;
 KW Wegener's granulomatosis; idiopathic pulmonary fibrosis; asthma;
 KW Graft-versus-host disease; leukemia; human.

XX Homo sapiens.

XX US2004131612-A1.

XX 08-JUL-2004.

XX 08-JAN-2003; 2003US-00338552.

XX 08-JAN-2003; 2003US-00338552.

XX (WATK/) WATKINS J D.

XX (VASS/) VASSEROT A P.

XX (MARQ/) MARQUIS D.

XX (HUSE/) HUSE W D.

XX

PI Watkins JD, Vasserot AP, Marquis D, Huse WD;

XX WPI; 2004-516978/49.

DR N-PSDB; ADQ80590.

XX Composition useful for treating diseases such as leukemia, asthma,
 PT rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple
 PT sclerosis, comprises TNF-alpha binding molecule.

XX Disclosure; SEQ ID NO 65; 60pp; English.

PS The invention relates to a composition which comprises a TNF-alpha
 CC binding molecule having sequence of complementarity determining region
 CC (CDR) in light chain variable region (CDRL)-3 and sequence of CDR in
 CC heavy chain variable region (CDRH)-3. The composition is useful in the
 CC treatment of TNF-alpha mediated diseases. TNF-alpha binding molecule is
 CC useful for treating sepsis, autoimmune disease, rheumatoid arthritis,
 CC allergy, multiple sclerosis, systemic lupus erythematosus, scleroderma,
 CC diabetes mellitus, cachexia, acute and chronic parasitic and/or
 CC infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, disseminated intravascular coagulation,
 CC Parkinson's disease, Alzheimer's disease, Down's syndrome, psoriasis,
 CC ankylosing spondylitis, Wegener's granulomatosis, idiopathic pulmonary
 CC fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha
 CC binding molecule is useful in diagnostic methods for detecting TNF-alpha
 CC in patients known to be or suspected of having TNF-alpha-mediated
 CC disease. TNF-alpha binding molecule is useful in immunoassays for
 CC detecting or quantifying TNF-alpha in a sample. The present sequence
 CC represents the amino acid sequence of a human heavy chain framework
 CC region.

XX Sequence 25 AA;

Query Match 100.0%; Score 123; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVSGGGLVPGGSLRLSCAAS 25
 |||||
 Db 1 EVQLVSGGGLVPGGSLRLSCAAS 25

RESULT 3

ADQ80699
 ID ADQ80699 standard; peptide; 25 AA.

XX ADQ80699;

XX 21-OCT-2004 (first entry)

XX Anti-VEGF antibody heavy chain FR1 subgroup III peptide SEQ ID NO:3.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytosstatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain; FR1.

XX Homo sapiens.

OS Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

Query Match 100.0%; Score 123; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 6
ADY31534
ID ADY31534 standard; peptide; 25 AA.
XX
AC ADY31534;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 366.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 366; 179pp; English.
XX
SQ The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework peptide.

Query Match 100.0%; Score 123; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 7
ADY31516
ID ADY31516 standard; peptide; 25 AA.
XX
AC ADY31516;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 348.
XX

DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 348; 179pp; English.
XX
SQ The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework peptide.

Query Match 100.0%; Score 123; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 8
ADY31483
ID ADY31483 standard; peptide; 25 AA.
XX
AC ADY31483;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody heavy chain framework peptide - SEQ ID 315.
XX
KW DNA library; humanized antibody; antibody engineering; heavy chain.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX

PT New library of nucleic acid sequences comprises nucleotide sequences
 PT encoding humanized heavy chain variable regions and humanized light chain
 PT variable regions, useful for producing humanized antibodies.

XX Disclosure; SEQ ID NO 315; 179pp; English.

XX The invention comprises a library of nucleotide sequences encoding
 CC humanized antibody heavy chain variable regions and humanized antibody
 CC light chain variable regions. The library of the invention is useful for
 CC producing humanized antibodies, or for re-engineering or reshaping an
 CC antibody from a first species for use in a second species. The present
 CC amino acid sequence represents a human germline heavy chain framework
 CC peptide.

XX Sequence 25 AA;

SQ Query Match 100.0%; Score 123; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 9
 ADY31489
 ID ADY31489 standard; peptide; 25 AA.

XX AC ADY31489;

XX DT 05-MAY-2005 (first entry)

XX Human antibody heavy chain framework peptide - SEQ ID 321.

XX DNA library; humanized antibody; antibody engineering; heavy chain.

XX Homo sapiens.

XX US2005042664-A1.

XX 24-FEB-2005.

XX 20-AUG-2004; 2004US-00923068.

XX 22-AUG-2003; 2003US-0497213P.

XX 13-OCT-2003; 2003US-0510741P.

XX (MEDI-) MEDIMUNE INC.

XX Wu H, Dall-Acqua W, Damschroder M;

XX WPI; 2005-180802/19.

XX New library of nucleic acid sequences comprises nucleotide sequences
 PT encoding humanized heavy chain variable regions and humanized light chain
 PT variable regions, useful for producing humanized antibodies.

XX Disclosure; SEQ ID NO 321; 179pp; English.

XX The invention comprises a library of nucleotide sequences encoding
 CC humanized antibody heavy chain variable regions and humanized antibody
 CC light chain variable regions. The library of the invention is useful for
 CC producing humanized antibodies, or for re-engineering or reshaping an
 CC antibody from a first species for use in a second species. The present
 CC amino acid sequence represents a human germline heavy chain framework
 CC peptide.

XX Sequence 25 AA;

SQ Query Match 100.0%; Score 123; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 10

ADY31540

ID ADY31540 standard; peptide; 25 AA.

XX AC ADY31540;

XX DT 05-MAY-2005 (first entry)

XX Human antibody heavy chain framework peptide - SEQ ID 372.

XX DNA library; humanized antibody; antibody engineering; heavy chain.

XX Homo sapiens.

XX US2005042664-A1.

XX 24-FEB-2005.

XX 20-AUG-2004; 2004US-00923068.

XX 22-AUG-2003; 2003US-0497213P.

XX 13-OCT-2003; 2003US-0510741P.

XX (MEDI-) MEDIMUNE INC.

XX Wu H, Dall-Acqua W, Damschroder M;

XX WPI; 2005-180802/19.

XX New library of nucleic acid sequences comprises nucleotide sequences
 PT encoding humanized heavy chain variable regions and humanized light chain
 PT variable regions, useful for producing humanized antibodies.

XX Disclosure; SEQ ID NO 372; 179pp; English.

XX The invention comprises a library of nucleotide sequences encoding
 CC humanized antibody heavy chain variable regions and humanized antibody
 CC light chain variable regions. The library of the invention is useful for
 CC producing humanized antibodies, or for re-engineering or reshaping an
 CC antibody from a first species for use in a second species. The present
 CC amino acid sequence represents a human germline heavy chain framework
 CC peptide.

XX Sequence 25 AA;

SQ Query Match 100.0%; Score 123; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 11

ADZ07629

ID ADZ07629 standard; peptide; 29 AA.

XX AC ADZ07629;

XX DT 16-JUN-2005 (first entry)

XX Mouse 3A6 antibody heavy chain, N-terminal sequence.

XX antibody; heavy chain; pharmaceutical; peripheral neuropathy;
 KW central nervous system disease; neurodegenerative disease;
 KW Alzheimers disease; Parkinsons disease; motor neurone disease;

ocular disease; diabetic retinopathy; age related macular degeneration;
myopia, cns-gen; neuroprotective; nootropic; antiparkinsonian;
antidiabetic; ophthalmological; 3A6.

Mus musculus.

WO2005028508-A2.

31-MAR-2005.

17-SEP-2004; 2004WO-EP010489.

19-SEP-2003; 2003GB-00021997.

(NOVS) NOVARTIS AG.

(NOVS) NOVARTIS PHARMA GMBH.

(UVZU-) UNIV ZURICH.

Bareke C, Frentzel S, Mir AK, Schwab ME, Vitaliti A;

WPI; 2005-242564/25.

New binding molecule capable of binding to human NogoA polypeptide, human NiG, human NiG-D20, or human NogoA342-357, useful for treating nerve repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral sclerosis.

Example 4; Page 30; 117pp; English.

The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable of binding to human NogoA polypeptide (SEQ ID NO: 5), human NiG polypeptide (SEQ ID NO: 7), human NiG-D20 polypeptide (SEQ ID NO: 24), or human NogoA 342-357 (SEQ ID NO: 6) all given in the specification, with a dissociation constant of less than 100nM. The binding molecule of the invention comprises a first antigen binding site comprising in sequence the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the hypervariable regions are at least 50% homologous to their equivalent hypervariable regions CDR-H1-3A6 (SEQ ID NO: 8), CDR-H2-3A6 (SEQ ID NO: 9), and CDR-H3-3A6 (SEQ ID NO: 10) all given in the specification, and a second antigen binding site comprising in sequence the hypervariable regions CDR-L1, CDR-L2, and CDR-L3, where each of the hypervariable regions are at least 50% homologous to their equivalent hypervariable regions CDR-L1-3A6 (SEQ ID NO: 11), CDR-L2-3A6 (SEQ ID NO: 12), and CDR-L3-3A6 (SEQ ID NO: 13) all given in the specification. Also described are: (i) polynucleotide sequences encoding the binding molecules above, (ii) polynucleotide sequences comprising fully defined sequences (SEQ ID Nos 14-19) given in the specification, (iii) an expression vector comprising the polynucleotide sequences above, where the expression system or its part is capable of producing a polypeptide, when the an isolated host cell comprising the expression system above, (iv) a pharmaceutical composition comprising the binding molecule in association with at least one pharmaceutical carrier or diluent, and (vi) a method of treating diseases associated with nerve repair. The binding molecules of the invention are useful as a pharmaceutical, preferably in the treatment of nerve repair. They are also useful in the treatment of various diseases of the peripheral (PNS) and central (CNS) nervous system, e.g. neurodegenerative diseases including Alzheimer's disease, Parkinson's disease, or amyotrophic lateral sclerosis. The binding molecules may also be used for treating degenerative ocular disorders including diabetic retinopathy, age-related macular degeneration, or pathologic myopia. This sequence represents the N-terminal sequence of the heavy chain of mouse 3A6 antibody as determined by sequence degradation.

Sequence 29 AA;

Query Match 100.0%; Score 123; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.4e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVSGGGLVQPGSRLRSCAAS 25
Db 1 EVQLVSGGGLVQPGSRLRSCAAS 25

RESULT 12

AAR87049
ID AAR87049 standard; peptide; 30 AA.

XX
AC AAR87049;

XX
DT 25-JUN-1996 (first entry)

XX
DE Human group III heavy chain framework 1.

XX
KW Humanised antibody; interleukin-5; IL-5; recombinant antibody;

XX
KW antibody engineering; monoclonal antibody; MAb; 39D10; CDR;

XX
KW complementarity determining region; heavy chain; framework; eosinophilia;

XX
KW allergy; asthma.

XX
OS Homo sapiens.

XX
PN WO9535375-A1.

XX
PD 28-DEC-1995.

XX
PF 16-JUN-1995; 95WO-GB001411.

XX
PR 17-JUN-1994; 94GB-00012230.

XX
PA (CLLT) CELLTECH THERAPEUTICS LTD.

XX
PI Entage JS, Bodmer MW, Athwal DS;

XX
DR WPI; 1996-058412/06.

XX
PT Anti-human IL-5 recombinant antibody - useful for preventing or reducing eosinophilia and for treating certain allergic diseases, esp. asthma.

XX
PS Example 3; Fig 4; 69pp; English.

XX
CC Framework regions (AAR87049-52) of human group III (gp3) germ line antibody heavy chain showed homology to corresponding regions (AAR87053-56, respectively) of the rat anti-human interleukin-5 monoclonal antibody 39D10 heavy chain (see AAR87039). This homology was utilised in the prodn. of a humanised 39D10 VH (AAR87058) in which rat 39D10 VH complementarity determining regions were grafted into the human gp3 framework

XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 123; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVSGGGLVQPGSRLRSCAAS 25

Db 1 EVQLVSGGGLVQPGSRLRSCAAS 25

RESULT 13

AAE19691

ID AAE19691 standard; peptide; 30 AA.

XX
AC AAE19691;

XX
DT 31-MAY-2002 (first entry)

XX
DE Human group 3 consensus peptide #1.

XX
KW Human: tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;

XX
KW complementarity determining region; rheumatoid; osteo-arthritis; sepsis;

XX
KW congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;

XX
KW Acquired immune deficiency syndrome; adult respiratory distress syndrome;

XX
KW cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;

XX
KW inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;

KW neoplasty therapy; immunomodulator; vulnery; graft rejection.

XX Homo sapiens.

XX WO200194585-A1.

XX 13-DEC-2001.

XX 05-JUN-2001; 2001WO-GB002477.

XX 06-JUN-2000; 2000GB-00013810.

XX (CELL-) CELLTech R & D LTD.

XX Athwal DS, Brown DT, Weir ANC, Popplewell AG, Chapman AP;

XX King DJ;

XX WPI; 2002-216732/27.

XX New antibody specific for human tumor necrosis factor (TNF)-alpha, useful
PT for treating TNF-alpha-mediated diseases, e.g. congestive heart failure,
XX septic or endotoxic shock, cachexia, adult respiratory distress syndrome.

XX Example 1; Fig 2; 119pp; English.

XX The invention relates to an antibody molecule having specificity for
CC human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light
CC chain. The antibody or the compound comprising the antibody is useful for
CC treating or manufacturing a medicament for treating a pathology mediated
CC by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated
CC diseases which can be treated by the antibody include sepsis, congestive
CC heart failure, septic or endotoxic shock, cachexia, adult respiratory
CC distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies,
CC psoriasis, tuberculosis, inflammatory bone disorders, blood coagulation
CC disorders, burns, rejection episodes following organ or tissue
CC transplant, Crohn's disease and autoimmune diseases, such as thyroiditis.
CC The antibodies may also be used to reduce the side effects associated
CC with TNFalpha generation during neoplasty therapy, to eliminate or reduce
CC shock-related symptoms associated with the treatment or prevention of
CC graft rejection by use of an anti-lymphocyte antibody, for treating multi
CC -organ failure, or in the diagnosis and imaging of disease states
CC involving elevated levels of TNF alpha. The present sequence is human
CC group 3 consensus peptide used in the exemplification of the invention

XX Sequence 30 AA;

Query Match 100.0%; Score 123; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 14

ADX27037

ID ADX27037 standard; peptide; 30 AA.

AC ADX27037;

XX 05-MAY-2005 (first entry)

XX Human group 3 consensus heavy chain framework region peptide - SEQ 106.

XX antibody; antiarthritic; antirheumatic; gastrointestinal-gen.;

XX antiinflammatory; rheumatoid arthritis; musculoskeletal disease;

XX inflammatory bowel disease; gastrointestinal disease; inflammation;

XX Crohns disease; immune disorder; heavy chain.

XX Homo sapiens.

XX WO2005014649-A2.

XX 17-FEB-2005.

XX 29-JUL-2004; 2004WO-IB002529.

XX 08-AUG-2003; 2003US-0493740P.

XX (PHAA) PHARMACIA CORP.

XX Banerjee A, Gustafson M, Ho SV, McLaughlin J, Thomas K;

XX WPI; 2005-152548/16.

XX Preparing a tumor necrosis factor-alpha antibody having a heavy and light
PT chain comprises fermenting a cell mixture, forming a cell pellet and
PT allowing the pellet to stand for a hold time.

XX Example 4; SEQ ID NO 106; 125pp; English.

XX The invention relates to a novel method for preparing an antibody with a
CC heavy and light chain comprising fermenting a cell mixture, where the
CC cells are capable of expressing the light and heavy chain, separating the
CC cells from the supernatant to form a cell pellet, allowing the pellet to
CC stand for a hold time, extracting the cell pellet and producing the TNF
CC (tumor necrosis factor)-alpha antibody fragment or its dimer or adduct.
CC The antibody of the invention demonstrates antiarthritic, antirheumatic,
CC gastrointestinal-gen. and antiinflammatory activities and may be useful
CC for treatment of rheumatoid arthritis or an inflammatory bowel disease,
CC such as Crohn's disease. Currently used anti-TNF-alpha monoclonal
CC antibodies, such as infliximab and etanercept, have limited success in
CC the treatment of disease since they must be administered frequently or
CC intravenously. Furthermore, both of these molecules comprise large
CC proteins and as such are difficult and expensive to manufacture. The
CC current sequence is that of a human group 3 consensus heavy chain
CC framework region peptide of the invention which may be used to construct
CC a chimeric antibody targeted to TNF-alpha.

XX Sequence 30 AA;

Query Match 100.0%; Score 123; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.6e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 15

ADY31384

ID ADY31384 standard; peptide; 30 AA.

AC ADY31384;

XX 05-MAY-2005 (first entry)

XX Human antibody heavy chain framework peptide - SEQ ID 216.

XX DNA library; humanized antibody; antibody engineering; heavy chain.

XX Homo sapiens.

XX US2005042664-A1.

XX 24-FEB-2005.

XX 20-AUG-2004; 2004US-00923068.

XX 22-AUG-2003; 2003US-0497213P.

XX 13-OCT-2003; 2003US-0510741P.

XX (MEDI-) MEDIMUNE INC.

XX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:15:41 ; Search time 21.2264 Seconds
(without alignments)
113.322 Million cell updates/sec

Title: US-10-764-428-3
Perfect score: 123
Sequence: 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	97	2 S26890	Ig heavy chain V r
2	123	100.0	97	2 S46462	Ig heavy chain V r
3	123	100.0	98	2 PL0121	Ig heavy chain V-I
4	123	100.0	98	2 S26894	Ig heavy chain V r
5	123	100.0	98	2 S29545	Ig heavy chain V r
6	123	100.0	98	2 S28934	Ig heavy chain V-I
7	123	100.0	98	2 PL0123	Ig heavy chain V r
8	123	100.0	98	2 S26891	Ig heavy chain V r
9	123	100.0	98	2 S26896	Ig heavy chain V r
10	123	100.0	98	2 S26933	Ig heavy chain V r
11	123	100.0	100	2 S28925	Ig heavy chain V r
12	123	100.0	100	2 S26926	Ig heavy chain V r
13	123	100.0	114	2 S36280	Ig heavy chain V-g
14	123	100.0	117	2 S17079	Ig heavy chain V r
15	123	100.0	117	2 S21980	Ig heavy chain V r
16	123	100.0	117	2 S36259	Ig heavy chain V r
17	123	100.0	117	2 A34964	Ig heavy chain pre
18	123	100.0	118	2 S31121	Ig heavy chain - h
19	123	100.0	119	1 GLHUTE	Ig heavy chain V-I
20	123	100.0	119	2 S31107	Ig heavy chain - h
21	123	100.0	120	1 M3HUBW	Ig heavy chain V-I
22	123	100.0	123	2 S26794	Ig heavy chain V r
23	123	100.0	123	2 S31509	Ig heavy chain - h
24	123	100.0	124	2 S20775	Ig heavy chain V r
25	123	100.0	125	2 S30531	Ig heavy chain V r
26	123	100.0	136	2 S31587	Ig heavy chain V r
27	123	100.0	139	2 I37781	Ig variable region
28	123	100.0	140	2 S26557	Ig heavy chain pre
29	123	100.0	143	2 S23624	Ig heavy chain V r

30	123	100.0	147	2 I37780	Ig variable region
31	123	100.0	191	2 JL0048	Ig heavy chain V r
32	122	99.2	116	2 B28966	Ig heavy chain pre
33	120	97.6	82	2 C34964	Ig heavy chain pre
34	120	97.6	98	2 S26889	Ig heavy chain V r
35	120	97.6	98	2 S54856	Ig heavy chain V-I
36	120	97.6	100	2 PL0122	Ig heavy chain V r
37	120	97.6	113	2 S25571	Ig heavy chains V-
38	120	97.6	115	1 H3HUTL	Ig heavy chain V-I
39	120	97.6	116	1 A1HUTU	Ig heavy chain V-I
40	120	97.6	117	1 G1HUMS	Ig heavy chain pre
41	120	97.6	117	1 H3HU26	Ig heavy chain pre
42	120	97.6	117	2 A45953	Ig heavy chain pre
43	120	97.6	117	2 B34964	Ig heavy chain pre
44	120	97.6	119	1 M3HUPM	Ig heavy chain V-I
45	120	97.6	119	2 D36005	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tolsonson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: UNIPARC:UPI00001138FA; EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PIR:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 2

S46462
Ig heavy chain V region (YAC-5) - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S46462
R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; W
Nature Genet. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46462
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <COO>
A:Cross-references: UNIPARC:UPI00001165D9; EMBL:Z27504; NID:g505430; PIDN:CAA81824.1; PIR:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

```
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||||
RESULT 3
PL0121
Ig heavy chain V-III region (TD-Vp) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C:Accession: PL0121
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0121
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>
A:Cross-references: UNIPARC:UPI0000176B97
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (TD-Vp) from one of five DNA rearrangements from
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match      100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 4
S26894
Ig heavy chain V region (DP-51) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26894
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI000002DD14; EMBL:Z12351; NID:g32924; PIDN:CAA78221.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 5
S29545
Ig heavy chain V region (COS 6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29545
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29545
```

```
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000116412; EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 6
S26934
Ig heavy chain V region (DP-59) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26934
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000116415; EMBL:Z12359; NID:g32937; PIDN:CAA78229.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 7
PL0123
Ig heavy chain V-III region (TD-Vr) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0123; S26897
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0123
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>
A:Cross-references: UNIPARC:UPI0000116413
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement f
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000116413; EMBL:Z12354; NID:g32930; PIDN:CAA78224.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
```


F,49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|

RESULT 8

S26891
Ig heavy chain V region (DP-58) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26891
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26891
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000116414; EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|

RESULT 9

S26896
Ig heavy chain V region (DP-53) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S26896
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26896
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000176866; EMBL:Z12353
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|

RESULT 10

S26933
Ig heavy chain V region (DP-40) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26933

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI000011640D; EMBL:Z12340; NID:g32902; PIDN:CAA78210.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|

RESULT 11

S26925
Ig heavy chain V region (DP-29) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26925
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26925
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <TOM>
A:Cross-references: UNIPARC:UPI0000116406; EMBL:Z12331; NID:g32879; PIDN:CAA78201.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F,15-100/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|

RESULT 12

S26926
Ig heavy chain V region (DP-30) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26926
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26926
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <TOM>
A:Cross-references: UNIPARC:UPI0000116407; EMBL:Z12332; NID:g32883; PIDN:CAA78202.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F,15-100/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 |||||
 Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 13

S36280
 Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C/Accession: S36280
 R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.
 A/Reference number: S36256; MUID:93178448; PMID:7679990
 A/Accession: S36280
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-114 <GRI>
 A/Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176D1E; EMBL:Z18822
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.3e-10; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 |||||
 Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 14

S17079
 Ig heavy chain V-gene (clone HHG19) - human
 C/Species: Homo sapiens (man)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C/Accession: S60299; S17079
 R/Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
 Immunol. Lett. 34, 57-62, 1992
 A/Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm

A/Reference number: S60295; MUID:93122853; PMID:1282498
 A/Accession: S60299
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-117 <KU2>
 A/Cross-references: UNIPARC:UPI0000115FF4; EMBL:X62128; NID:G38340; PIDN:CAA44059.1; PID
 A/Note: the authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72,
 C/Genetics:
 A/Introns: 16/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 |||||
 Db 20 EVQLVESGGGLVQPGGSLRLSCAAS 44

RESULT 15

S21980
 Ig heavy chain V-gene (clone WHG26) precursor - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
 C/Accession: S60295; S21980
 R/Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
 Immunol. Lett. 34, 57-62, 1992
 A/Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm

A/Reference number: S60295; MUID:93122853; PMID:1282498
 A/Accession: S60295
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-117 <KU2>
 A/Cross-references: UNIPARC:UPI0000115FF6; EMBL:X62130; NID:G38344; PIDN:CAA44061.1; PID
 C/Genetics:
 A/Introns: 16/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 123; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.4e-10; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
 |||||
 Db 20 EVQLVESGGGLVQPGGSLRLSCAAS 44

Search completed: April 25, 2006, 06:26:12
 Job time : 22.2264 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 133,491 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-3
Perfect score: 123
Sequence: 1 EVQLVSGGGLVQPGGSLRLSCAAS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	118	Q9UL72_HUMAN	Q9UL72 homo sapien
2	123	100.0	118	Q9UL91_HUMAN	Q9UL91 homo sapien
3	123	100.0	119	HV3P_HUMAN	P01777 homo sapien
4	123	100.0	120	HV3E_HUMAN	P01766 homo sapien
5	123	100.0	478	Q6PI81_HUMAN	Q6PI81 homo sapien
6	123	100.0	479	Q6MZV6_HUMAN	Q6MZV6 homo sapien
7	123	100.0	493	Q6GMX2_HUMAN	Q6GMX2 homo sapien
8	122	99.2	116	HV05_CARAU	P19181 carassius a
9	122	99.2	473	Q6MZV7_HUMAN	Q6MZV7 homo sapien
10	120	97.6	113	Q9UL90_HUMAN	Q9UL90 homo sapien
11	120	97.6	115	HV3D_HUMAN	P01765 homo sapien
12	120	97.6	116	HV3C_HUMAN	P01779 homo sapien
13	120	97.6	117	HV3C_HUMAN	P01764 homo sapien
14	120	97.6	117	HV3O_HUMAN	P01776 homo sapien
15	120	97.6	119	HV3M_HUMAN	P01774 homo sapien
16	120	97.6	466	Q6N096_HUMAN	Q6N096 homo sapien
17	120	97.6	465	Q6MZQ6_HUMAN	Q6MZQ6 homo sapien
18	120	97.6	521	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
19	120	97.6	597	Q96BB9_HUMAN	Q96BB9 homo sapien
20	119	96.7	115	HV3F_HUMAN	P01767 homo sapien
21	119	96.7	131	Q9UL88_HUMAN	Q9UL88 homo sapien
22	119	96.7	464	Q6MZU6_HUMAN	Q6MZU6 homo sapien
23	119	96.7	470	Q7Z5W1_HUMAN	Q7Z5W1 homo sapien
24	119	96.7	475	Q6GMW7_HUMAN	Q6GMW7 homo sapien
25	119	96.7	494	Q96K68_HUMAN	Q96K68 homo sapien
26	117	95.1	240	Q65ZC9_HUMAN	Q65ZC9 homo sapien
27	116	94.3	98	HV57_MOUSE	P18528 mus musculus
28	116	94.3	115	HV3S_HUMAN	P01780 homo sapien
29	116	94.3	117	HV54_MOUSE	P18525 mus musculus
30	116	94.3	117	HV55_MOUSE	P18526 mus musculus
31	116	94.3	119	Q5F2I8_MOUSE	Q5F2I8 mus musculus

RESULT 1

ID	Q9UL72_HUMAN	PRELIMINARY;	PRT;	118 AA.
AC	Q9UL72;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.W.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
RN	[2]			
RP	PROTEIN SEQUENCE.			
RX	PubMed=1555592;			
RA	Makiya R., Stigbrand T.;			
RT	"Placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion.";			
RL	Bur. J. Biochem. 205:341-345(1992).			
DR	EMBL; AF035042; AAD56278.1; -; mRNA.			
DR	PIR; S21205; S21205.			
DR	HSP; P01783; IIGC.			
DR	SMR; Q9UL72; 1-118.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER 1			
FT	NON_TER 118			
SQ	SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;			

Query Match 100.0%; Score 123; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
|||||
DB 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
|||||

RESULT 2

ID	Q9UL91_HUMAN	PRELIMINARY;	PRT;	118 AA.
AC	Q9UL91;			

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652 (1991).
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed=155592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345 (1992).
DR EMBL; AF035023; AAD56259.1; -; mRNA.
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSSP; P01783; IIGC.
DR SMR; Q0UL91; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 100.0%; Score 123; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 3
HV3P HUMAN
ID HV3P HUMAN STANDARD; PRT; 119 AA.
AC P01777;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region TBI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;

Query Match 100.0%; Score 123; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 4
HV3E HUMAN
ID HV3E HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999 (1976).
CC -!- MISCELLANEOUS: This chain was obtained from IgM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenström
CC type.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A02049; M3HUBW.
DR HSSP; P01783; IIGC.
DR SMR; P01766; 1-120.
```

```
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup; definitive identification of four heavy chain
RT hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848 (1974).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A02060; G1HUTE.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 107 Ig-like.
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 12803 MW; 7E24DC852C7290A9 CRC64;

Query Match 100.0%; Score 123; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 4
HV3E HUMAN
ID HV3E HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999 (1976).
CC -!- MISCELLANEOUS: This chain was obtained from IgM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenström
CC type.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A02049; M3HUBW.
DR HSSP; P01783; IIGC.
DR SMR; P01766; 1-120.
```

DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin v region.
 FT DOMAIN 1 111 Ig-like.
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13227 MW; D3F042887C2B6410 CRC64;
 Query Match 100.0%; Score 123; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EVLVESGGGLVQPGGSLRLSCAAS 25
 Db 1 EVLVESGGGLVQPGGSLRLSCAAS 25
 RESULT 5
 Q6PI81 HUMAN PRELIMINARY; PRT; 478 AA.
 ID Q6PI81
 AC Q6PI81
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein
 GN Name=IGHM; Human
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC041037; AAH41037.1; -, mRNA.
 DR HSSP: P01861; IADQ.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG v.
 Pfam: PF07654; Cl-set; 3.

DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;
 Query Match 100.0%; Score 123; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EVLVESGGGLVQPGGSLRLSCAAS 25
 Db 20 EVLVESGGGLVQPGGSLRLSCAAS 44
 RESULT 6
 Q6MZV6 HUMAN PRELIMINARY; PRT; 479 AA.
 ID Q6MZV6
 AC Q6MZV6
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686L19235.
 GN Name=DKFZp686L19235;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human small intestine;
 RG The German Human cDNA Consortium;
 RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640854; CAB45921.1; -, mRNA.
 DR HSSP: P01842; IADQ.
 DR SMR: Q6MZV6; 249-457.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig c1.
 DR InterPro: IPR003598; IG c2.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG v.
 Pfam: PF07654; Cl-set; 2.
 DR SMART: SM00409; IG; 4.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 51639 MW; 6FA495DF0AA71DD4 CRC64;
 Query Match 100.0%; Score 123; DB 2; Length 479;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EVLVESGGGLVQPGGSLRLSCAAS 25
 Db 20 EVLVESGGGLVQPGGSLRLSCAAS 44
 RESULT 7
 Q6GMX2 HUMAN PRELIMINARY; PRT; 493 AA.
 ID Q6GMX2
 AC Q6GMX2
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHA1 protein.

```

GN Name=IGHAL;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073771; AAH73771.1; -; mRNA.
DR SMR; O6GMK2; 263-471.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;

Query Match 100.0%; Score 123; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVPGGSLRLSCAAS 25
DB |||||
20 EVQLVSGGGLVPGGSLRLSCAAS 44

RESULT 8
HV05 CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain v region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073771; AAH73771.1; -; mRNA.
DR SMR; O6GMK2; 263-471.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;

Query Match 100.0%; Score 123; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVPGGSLRLSCAAS 25
DB |||||
20 EVQLVSGGGLVPGGSLRLSCAAS 44

RESULT 8
HV05 CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain v region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]

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DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476RAB4C0BFC447 CRC64;

Query Match 99.2%; Score 122; DB 2; Length 473;
Best Local Similarity 96.0%; Pred. No. 9.9e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
Db 20 EIQLVSGGGLVQPGGSLRLSCAAS 44

RESULT 10
Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2F84.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 113 113
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 97.6%; Score 120; DB 2; Length 113;
Best Local Similarity 96.0%; Pred. No. 4.5e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVSGGGLVQPGGSLRLSCAAS 25

RESULT 11
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE "Variable region sequences of five human immunoglobulin heavy chains
DE of the VH3 subgroup; definitive identification of four heavy chain
DE hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -!- MISCELLANEOUS: This chain was isolated from an IgA1 myeloma
CC protein.

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CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR PIR; A02062; A1HTU1.
DR HSP; P01783; IIGC.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112 Ig-like.
FT NON_TER 116 116
FT SEQUENCE 116 AA; 12431 MW; EB705F53A963F0C CRC64;
Query Match 97.6%; Score 120; DB 1; Length 116;
Best Local Similarity 96.0%; Pred. No. 4.6e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
||||:|||||
1 EVQLVESGGGLVQPGGSLRLSCAAS 25
1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 13
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
[2]
RN NUCLEOTIDE SEQUENCE OF 20-117.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Tsapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human
RT monoclonal IgM with an antibody activity to myelin-associated
RT glycoprotein.";
RL Eur. J. Immunol. 23:846-851(1993).
[3]
RN 3D-STRUCTURE MODELING OF 20-117.
RX MEDLINE=86094276; PubMed=3866244;
RA Toyonaga B., Yoshikai Y., Vadasz V., Chin B., Mak T.W.;
RT "Organization and sequences of the diversity, joining, and constant
RT region genes of the human T-cell receptor beta chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC
CC EMBL; J00236; AA53516.1; -; Unassigned DNA.
CC EMBL; M35415; AA58735.1; -; Genomic DNA.
CC PIR; A02047; H3HU26.
CC PDB; 1HOU; Model; R=20-117.
CC HGNC; HGNC:5545; IGHV@.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V-III region VH26.
FT DOMAIN 20 >117 Ig-like.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
Query Match 97.6%; Score 120; DB 1; Length 117;
Best Local Similarity 96.0%; Pred. No. 4.7e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 20 EVQLVESGGGLVQPGGSLRLSCAAS 44
||||:|||||
1 EVQLVESGGGLVQPGGSLRLSCAAS 25
20 EVQLVESGGGLVQPGGSLRLSCAAS 44

RESULT 14
HV3O_HUMAN
ID HV3O_HUMAN STANDARD; PRT; 117 AA.
AC P01776;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region WAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A02059; GIHWS.
CC HSP; P01772; 2FB4.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112 Ig-like.

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FT NON TER 117 117
SQ SEQUENCE 117 AA; 13091 MW; 201DEF0B1E53D9BF CRC64;

Query Match 97.6%; Score 120; DB 1; Length 117;
Best Local Similarity 96.0%; Pred. No. 4.7e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 15
HV3M_HUMAN
ID HV3M_HUMAN STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region PWM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M anti-gamma
RT globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -!- MISCELLANEOUS: This chain was isolated from IgM with anti-gamma
CC globulin activity.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02057; M3HUPM.
DR HSSP; P01772; 2FB4.
DR SMR; P01774; 1-119.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0008555; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT VARIANT 54 54
FT FTID=VAR_003966.
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12954 MW; 2E018AF4DCBB2610 CRC64;

Query Match 97.6%; Score 120; DB 1; Length 119;
Best Local Similarity 96.0%; Pred. No. 4.8e-09;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 33.7264 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-3

Perfect score: 123

Sequence: 1 EVQLVSGGGLVQPGGSLRLSCAAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/1aa/5 COMB.pcp.*
- 2: /cgm2_6/ptodata/1/1aa/6 COMB.pcp.*
- 3: /cgm2_6/ptodata/1/1aa/7 COMB.pcp.*
- 4: /cgm2_6/ptodata/1/1aa/8 COMB.pcp.*
- 5: /cgm2_6/ptodata/1/1aa/9 COMB.pcp.*
- 6: /cgm2_6/ptodata/1/1aa/10 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	26	1 US-08-471-780C-80	Sequence 80, Appl
2	123	100.0	26	1 US-08-467-282B-80	Sequence 80, Appl
3	123	100.0	26	1 US-08-471-282A-80	Sequence 80, Appl
4	123	100.0	26	1 US-08-466-710C-80	Sequence 80, Appl
5	123	100.0	26	2 US-08-468-739C-80	Sequence 80, Appl
6	123	100.0	26	2 US-09-293-769A-80	Sequence 80, Appl
7	123	100.0	26	1 US-08-537-871A-4	Sequence 4, Appl
8	123	100.0	30	1 US-08-470-139-17	Sequence 17, Appl
9	123	100.0	30	2 US-09-347-061-17	Sequence 17, Appl
10	123	100.0	30	2 US-09-855-271-17	Sequence 17, Appl
11	123	100.0	97	2 US-10-194-975-18	Sequence 18, Appl
12	123	100.0	97	2 US-10-194-975-31	Sequence 31, Appl
13	123	100.0	97	2 US-09-534-717-638	Sequence 638, App
14	123	100.0	98	1 US-08-211-202-116	Sequence 116, Appl
15	123	100.0	98	1 US-07-942-245-37	Sequence 37, Appl
16	123	100.0	98	1 US-08-665-202-31	Sequence 31, Appl
17	123	100.0	98	2 US-09-315-574-31	Sequence 31, Appl
18	123	100.0	98	2 US-10-194-975-15	Sequence 15, Appl
19	123	100.0	98	2 US-10-194-975-28	Sequence 28, Appl
20	123	100.0	98	2 US-10-194-975-30	Sequence 30, Appl
21	123	100.0	98	2 US-10-194-975-33	Sequence 33, Appl
22	123	100.0	98	2 US-09-534-717-611	Sequence 611, App
23	123	100.0	98	2 US-09-534-717-612	Sequence 612, App
24	123	100.0	98	2 US-09-534-717-613	Sequence 613, App
25	123	100.0	98	2 US-09-534-717-622	Sequence 622, App
26	123	100.0	98	2 US-09-534-717-639	Sequence 639, App
27	123	100.0	98	2 US-09-534-717-656	Sequence 656, App

ALIGNMENTS

RESULT 1

US-08-471-780C-80

; Sequence 80, Application US/08471780C

; Patent No. 5759808

; GENERAL INFORMATION:

; APPLICANT: Casterman, Cecile

; APPLICANT: Hamers, Raymond

; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains

; NUMBER OF SEQUENCES: 130

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,780C

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/106,944

; FILING DATE: 17-AUG-1993

; APPLICATION NUMBER: FR 92402326.0

; FILING DATE: 21-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 93401310.3

; FILING DATE: 21-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Potter, Jane E.R.

; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 04958.0008-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 80:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Camelus dromedarius

; US-08-471-780C-80

Sequence 660, App
Sequence 662, App
Sequence 663, App
Sequence 664, App
Sequence 665, App
Sequence 666, App
Sequence 32, Appl
Sequence 594, App
Sequence 595, App
Sequence 596, App
Sequence 4, Appl
Sequence 9, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 11, Appl


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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Camelus dromedarius
US-08-466-710C-80

Query Match 100.0%; Score 123; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 5
US-08-468-739C-80
Sequence 80, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
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FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Camelus dromedarius
US-08-468-739C-80

Query Match 100.0%; Score 123; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 6
US-09-293-769A-80
Sequence 80, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 80
LENGTH: 26
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Camelus sp. or
OTHER INFORMATION: Lama sp.
US-09-293-769A-80

Query Match 100.0%; Score 123; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 7
US-08-537-871A-4
Sequence 4, Application US/08537871A
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Patent No. 6838254
GENERAL INFORMATION:
APPLICANT: Raymond HAMERS
APPLICANT: Cecile HAMERS-CASSTERMAN
APPLICANT: Serge V. M. MUYLDERMANS
APPLICANT: Leon G. J. FRENKEN
APPLICANT: Cornelis T. VERIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: fragments thereof derived from heavy chain immunoglobulins
TITLE OF INVENTION: of Camelidae
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01442
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93202079.5
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93201454.1
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93201239.6
FILING DATE: 29-APR-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: human heavy chain framework (subgroup III)
US-08-537-871A-4
Query Match 100.0%; Score 123; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
RESULT 8
US-08-470-139-17
Sequence 17, Application US/08470139
Patent No. 598586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139

FILING DATE: 06 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-139-17
Query Match 100.0%; Score 123; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
RESULT 9
US-09-347-061-17
Sequence 17, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Entage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Consensus
US-09-347-061-17
Query Match 100.0%; Score 123; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
Db 1 EVQLVSGGGLVQPGGSLRLSCAAS 25
RESULT 10
US-09-855-271-17
Sequence 17, Application US/09855271
Patent No. 6734286
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark W
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Entage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0088
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/347,061
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17

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; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-09-855-271-17

Query Match      100.0%; Score 123; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 11
US-10-194-975-18
; Sequence 18, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-18

Query Match      100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
      |||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 12
US-10-194-975-31
; Sequence 31, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-31

Query Match      100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
      |||||
Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

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RESULT 13
US-09-534-717-638
; Sequence 638, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-638

Query Match      100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Db      1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 14
US-08-211-202-116
; Sequence 116, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSER: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883

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Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Search completed: April 25, 2006, 06:28:40
Job time : 34.7264 secs

Query Match 100.0%; Score 123; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 15

US-07-942-245-37

; Sequence 37, Application US/07942245

; Patent No. 5639641

; GENERAL INFORMATION:

; APPLICANT: PEDERSEN, Jan T.

; APPLICANT: SEARLE, Stephen M.J.

; APPLICANT: REES, Anthony R.

; APPLICANT: ROGUSKA, Michael A.

; APPLICANT: GUILD, Braydon C.

; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 522

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas

; STREET: 2100 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: United States

; ZIP: 20037-3202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: HP 9000/700 Workstation

; OPERATING SYSTEM: UNIX

; SOFTWARE: in house

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/942,245

; FILING DATE: 09-SEP-1992

; CLASSIFICATION: 530

; TELEPHONE: (202) 293-7060

; TELEFAX: (202) 293-7860

; TELEX: 6491103

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 98 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-942-245-37

Query Match 100.0%; Score 123; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Query Match 100.0%; Score 123; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 3
US-10-764-428-3
; Sequence 3, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; TITLE OF INVENTION: CULTURE
; FILE REFERENCE: 11669.120USU1
; CURRENT APPLICATION NUMBER: US/10/764,428
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FRI SGIII
US-10-764-428-3

Query Match 100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 4
US-10-923-068-315
; Sequence 315, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-315

Query Match 100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 5

US-10-923-068-321
; Sequence 321, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-321

Query Match 100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 6
US-10-923-068-339
; Sequence 339, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-339

Query Match 100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 7
US-10-923-068-348
; Sequence 348, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 25

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-348

Query Match      100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGSLRLSCAAS 25
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Db 1 EVLVESGGGLVQPGSLRLSCAAS 25

RESULT 8
US-10-923-068-363
; Sequence 363, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 363
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-363

Query Match      100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGSLRLSCAAS 25
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Db 1 EVLVESGGGLVQPGSLRLSCAAS 25

RESULT 9
US-10-923-068-366
; Sequence 366, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-366

Query Match      100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGSLRLSCAAS 25
   |||||
Db 1 EVLVESGGGLVQPGSLRLSCAAS 25

RESULT 10
US-10-923-068-372
; Sequence 372, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-372

Query Match      100.0%; Score 123; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGSLRLSCAAS 25
   |||||
Db 1 EVLVESGGGLVQPGSLRLSCAAS 25

RESULT 11
US-10-751-826-80
; Sequence 80, Application US/10751826
; Publication No. US20040253638A1
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/10/751,826
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/293,769A
; PRIOR FILING DATE: 1999-04-19
; PRIOR FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1987-10-15
; PRIOR FILING DATE: 1987-10-15
; PRIOR FILING DATE: 1992-08-21
; PRIOR FILING DATE: 1992-08-21
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Camelus sp. or
; OTHER INFORMATION: Lama sp.
US-10-751-826-80

Query Match      100.0%; Score 123; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGSLRLSCAAS 25
   |||||
Db 1 EVLVESGGGLVQPGSLRLSCAAS 25

RESULT 12
US-10-915-490-4
; Sequence 4, Application US/10915490
; Publication No. US20050130266A1
; GENERAL INFORMATION:
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; SEQ ID NO 121
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 3 consensus framework H1
US-09-875-221A-121

Query Match      100.0%; Score 123; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.4e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
        |||||
Db       1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Search completed: April 25, 2006, 07:08:48
Job time : 109.962 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds
(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-3

Perfect score: 123

Sequence: 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	30	7 US-11-004-590-113	Sequence 113, App
2	123	100.0	44	6 US-10-982-357-39	Sequence 39, Appl
3	123	100.0	87	6 US-10-982-357-46	Sequence 46, Appl
4	123	100.0	97	7 US-11-054-669-18	Sequence 18, Appl
5	123	100.0	97	7 US-11-054-669-31	Sequence 31, Appl
6	123	100.0	97	7 US-11-084-554-28	Sequence 28, Appl
7	123	100.0	97	7 US-11-004-590-17	Sequence 17, Appl
8	123	100.0	97	7 US-11-004-590-34	Sequence 34, Appl
9	123	100.0	97	7 US-11-136-250-28	Sequence 28, Appl
10	123	100.0	98	7 US-11-054-669-15	Sequence 15, Appl
11	123	100.0	98	7 US-11-054-669-28	Sequence 28, Appl
12	123	100.0	98	7 US-11-054-669-30	Sequence 30, Appl
13	123	100.0	98	7 US-11-054-669-33	Sequence 33, Appl
14	123	100.0	98	7 US-11-084-554-30	Sequence 30, Appl
15	123	100.0	98	7 US-11-084-554-36	Sequence 36, Appl
16	123	100.0	98	7 US-11-084-554-39	Sequence 39, Appl
17	123	100.0	98	7 US-11-084-554-44	Sequence 44, Appl
18	123	100.0	98	7 US-11-084-554-47	Sequence 47, Appl
19	123	100.0	98	7 US-11-004-590-14	Sequence 14, Appl
20	123	100.0	98	7 US-11-004-590-19	Sequence 19, Appl
21	123	100.0	98	7 US-11-004-590-27	Sequence 27, Appl
22	123	100.0	98	7 US-11-004-590-30	Sequence 30, Appl
23	123	100.0	98	7 US-11-004-590-33	Sequence 33, Appl
24	123	100.0	98	7 US-11-004-590-37	Sequence 37, Appl
25	123	100.0	98	7 US-11-136-250-30	Sequence 30, Appl

26	123	100.0	98	7	US-11-136-250-36	Sequence 36, Appl
27	123	100.0	98	7	US-11-136-250-39	Sequence 39, Appl
28	123	100.0	98	7	US-11-136-250-44	Sequence 44, Appl
29	123	100.0	98	7	US-11-136-250-47	Sequence 47, Appl
30	123	100.0	100	7	US-11-054-669-32	Sequence 32, Appl
31	123	100.0	100	7	US-11-084-554-45	Sequence 45, Appl
32	123	100.0	100	7	US-11-004-590-35	Sequence 35, Appl
33	123	100.0	100	7	US-11-136-250-45	Sequence 45, Appl
34	123	100.0	100	7	US-11-136-250-58	Sequence 58, Appl
35	123	100.0	109	7	US-11-155-843-68	Sequence 68, Appl
36	123	100.0	109	7	US-11-155-843-70	Sequence 70, Appl
37	123	100.0	109	7	US-11-155-843-71	Sequence 71, Appl
38	123	100.0	109	7	US-11-155-843-72	Sequence 72, Appl
39	123	100.0	109	7	US-11-155-843-73	Sequence 73, Appl
40	123	100.0	109	7	US-11-155-843-74	Sequence 74, Appl
41	123	100.0	109	7	US-11-155-843-75	Sequence 75, Appl
42	123	100.0	109	7	US-11-155-843-76	Sequence 76, Appl
43	123	100.0	109	7	US-11-155-843-77	Sequence 77, Appl
44	123	100.0	109	7	US-11-155-843-78	Sequence 78, Appl
45	123	100.0	109	7	US-11-155-843-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1

US-11-004-590-113

; Sequence 113, Application US/11004590

; Publication No. US2006000883A1

; GENERAL INFORMATION:

; APPLICANT: Lazar, Gregory Alan

; APPLICANT: Desjarlais, John R.

; APPLICANT: Hammond, Phillip W.

; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRAIN

; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

; FILE REFERENCE: 185832/US/5

; CURRENT APPLICATION NUMBER: US/11/004,590

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527,167

; PRIOR FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: US 60/581,613

; PRIOR FILING DATE: 2004-06-21

; PRIOR APPLICATION NUMBER: US 60/601,665

; PRIOR FILING DATE: 2004-08-13

; PRIOR APPLICATION NUMBER: US 60/619,483

; PRIOR FILING DATE: 2004-10-14

; NUMBER OF SEQ ID NOS: 458

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 113

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-004-590-113

Query Match 100.0%; Score 123; DB 7; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.8e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESULT 2

US-10-982-357-39

; Sequence 39, Application US/10982357

; Publication No. US20060024296A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs

; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/982,357

; CURRENT FILING DATE: 2004-11-05

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; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-357-39

Query Match      100.0%; Score 123; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGGSLRLSAAAS 25
Db 1 EVLVESGGGLVQPGGSLRLSAAAS 25

RESULT 3
US-10-982-357-46
; Sequence 46, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-357-46

Query Match      100.0%; Score 123; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGGSLRLSAAAS 25
Db 1 EVLVESGGGLVQPGGSLRLSAAAS 25

RESULT 4
US-11-054-669-18
; Sequence 18, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-18

Query Match      100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGGSLRLSAAAS 25
Db 1 EVLVESGGGLVQPGGSLRLSAAAS 25

RESULT 5
US-11-054-669-31
; Sequence 31, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-31

Query Match      100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGGSLRLSAAAS 25
Db 1 EVLVESGGGLVQPGGSLRLSAAAS 25

RESULT 6
US-11-084-554-28
; Sequence 28, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-28

Query Match      100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVQPGGSLRLSAAAS 25
Db 1 EVLVESGGGLVQPGGSLRLSAAAS 25

RESULT 7
US-11-004-590-17
; Sequence 17, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
```



```

; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-004-590-17

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Query Match      100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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pH 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||

RESULT 8

RES-11-004-590-34
 ; Sequence 34, Application US/11004590
 ; Publication NO. US2006008883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazar, Gregory Alan
 ; APPLICANT: Desjarlais, John R.
 ; APPLICANT: Hammond, Phillip W.
 ; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
 ; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
 ; FILE REFERENCE: 185832/US/5
 ; CURRENT APPLICATION NUMBER: US/11/004,590
 ; CURRENT FILING DATE: 2004-12-03
 ; PRIOR APPLICATION NUMBER: US 60/527,167
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/581,613
 ; PRIOR FILING DATE: 2004-06-21
 ; PRIOR APPLICATION NUMBER: US 60/601,665
 ; PRIOR FILING DATE: 2004-08-13
 ; PRIOR APPLICATION NUMBER: US 60/619,483
 ; PRIOR FILING DATE: 2004-10-14
 ; NUMBER OF SEQ ID NOS: 458
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 34
 ; LENGTH: 97
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; RES-11-004-590-34

Query Match 100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.e-09;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||
pH 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||

RESULT 9

US-11-136-250-28
: Sequence 28. Application US/11136250

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; Publication No. US20060021074A1
;
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirdid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
;
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
;
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-136-250-28

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Query Match 100.0%; Score 123; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels

[illegible]

RESULT 10

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US-11-054-669-15
Sequence 15, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patent in version 3.3
SEQ ID NO 15
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-669-15

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Query Match 100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
|||
nH 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

RESIM,T 11

; US-11-054-669-28
 ; Sequence 28, Application US/11054669
 ; Publication No. US20050261480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Foote, Jefferson
 ; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES

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; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-28

Query Match      100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||

RESULT 12
US-11-054-669-30
; Sequence 30, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-30

Query Match      100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||

RESULT 13
US-11-054-669-33
; Sequence 33, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 98

; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-33

Query Match      100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||

RESULT 14
US-11-084-554-30
; Sequence 30, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-30

Query Match      100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||
DB 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
   |||||

RESULT 15
US-11-084-554-36
; Sequence 36, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-36

Query Match      100.0%; Score 123; DB 7; Length 98;
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAS 25
| | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

Search completed: April 25, 2006, 07:10:01
Job time : 16.2044 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:15:41 ; Search time 8.49057 Seconds
(without alignments)
113.322 Million cell updates/sec

Title: US-10-764-428-14
Perfect score: 58
Sequence: 1 GYFTNYGIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	140	2	A36194
2	55	94.8	93	2	C24672
3	55	94.8	99	2	S26326
4	55	94.8	101	2	D24672
5	55	94.8	105	2	S24764
6	55	94.8	105	2	S24765
7	55	94.8	109	2	S26325
8	55	94.8	115	2	S19968
9	55	94.8	115	2	S19967
10	55	94.8	118	2	S19965
11	55	94.8	119	2	A53285
12	55	94.8	120	2	B24848
13	55	94.8	124	2	PH1404
14	55	94.8	146	4	S33905
15	53	91.4	76	2	B28572
16	53	91.4	98	2	B24754
17	53	91.4	98	2	A28572
18	53	91.4	102	2	PH1491
19	53	91.4	102	2	PH1490
20	53	91.4	114	2	PH1523
21	53	91.4	114	2	PH1522
22	53	91.4	118	2	S38565
23	53	91.4	118	2	A24754
24	53	91.4	119	2	PH1510
25	53	91.4	119	2	PH1505
26	53	91.4	119	2	PH1518
27	53	91.4	119	2	PH1517
28	53	91.4	119	2	PH1502
29	53	91.4	119	2	PH1500

ALIGNMENTS

RESULT 1

A36194
Ig heavy chain V region (clone 2B4.1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 16-Aug-1996
C:Accession: A36194
R:Gerstein, R.M.; Frankel, W.N.; Hsieh, C.L.; Durdik, J.M.; Rath, S.; Coffin, J.M.; Nisio Cell 63, 537-548, 1990
A:Title: Isotype switching of an immunoglobulin heavy chain transgene occurs by DNA recombination
A:Reference number: A36194; MUID:91029486; PMID:2121365
A:Accession: A36194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GER>
A:Cross-references: UNIPARC:UPI0000176C50; GB:M38389
A:Note: the protein sequence was not shown in this paper
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 58; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
|||||
Db 45 GYFTNYGIN 54

RESULT 2

C24672
Ig heavy chain V region (VMU-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C:Accession: C24672
R:Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A:Reference number: A91022; MUID:86055722; PMID:2998759
A:Accession: C24672
A:Molecule type: DNA
A:Residues: 1-93 <WIN>
A:Cross-references: UNIPARC:UPI0000113757; GB:X03300; NID:952375; PIDN:CAA27039.1; PID:952375; PIDN:CAA27039.1; PID:952375
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 94.8%; Score 55; DB 2; Length 93;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
|||||

Db 7 GYTFTNYGMN 16

RESULT 3

S26326
Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C/Accession: S26326
R/Starck, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein e
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26326
A/Molecule type: mRNA
A/Residues: 1-99 <STA>
A/Cross-references: UNIPARC:UPI00001769AC; EMBL:X59174
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.8%; Score 55; DB 2; Length 99;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10

|||||||:|

Db 6 GYTFTNYGMN 15

RESULT 4

D24672
Ig heavy chain V region (VGM3-8) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C/Accession: D24672
R/Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A/Reference number: A91022; MUID:86055722; PMID:2998759
A/Accession: D24672
A/Molecule type: DNA
A/Residues: 1-101 <WLN>
A/Cross-references: UNIPARC:UPI0000113758; GB:X03301; NID:q51757; PIDN:CAA27040.1; PID:q
A/Note: this sequence was determined from the differentiated gene
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.8%; Score 55; DB 2; Length 101;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10

|||||||:|

Db 7 GYTFTNYGMN 16

RESULT 5

S24764
Ig heavy chain V region (subgroup XI) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C/Accession: S24764; S24772; S24777

R/Klages, S.

submitted to the EMBL Data Library, August 1992
A/Reference number: S24763
A/Accession: S24764
A/Molecule type: DNA
A/Residues: 1-105 <KLA>
A/Cross-references: UNIPARC:UPI000011648C; EMBL:Z14999
A/Accession: S24772
A/Molecule type: DNA
A/Residues: 1-105 <KWL>
A/Cross-references: UNIPARC:UPI000011648C; EMBL:Z15011
R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776
A/Accession: S24777
A/Molecule type: DNA
A/Residues: 1-105 <THO>
A/Cross-references: UNIPARC:UPI000011648C; EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID
C/Genetics:
A/Introns: 9/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.8%; Score 55; DB 2; Length 105;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10

|||||||:|

Db 38 GYTFTNYGMN 47

RESULT 6

S24765
Ig heavy chain V region (subgroup XI) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C/Accession: S24765; S24773; S24778

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763
A/Accession: S24765
A/Molecule type: DNA
A/Residues: 1-105 <KLA>
A/Cross-references: UNIPARC:UPI000011648B; EMBL:Z15001
A/Accession: S24773
A/Molecule type: DNA
A/Residues: 1-105 <KLW>
A/Cross-references: UNIPARC:UPI000011648B; EMBL:Z15013
R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776
A/Accession: S24778
A/Molecule type: DNA
A/Residues: 1-105 <THO>
A/Cross-references: UNIPARC:UPI000011648B; EMBL:Z15022; NID:g52619; PIDN:CAA78741.1; PID
C/Genetics:
A/Introns: 9/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 94.8%; Score 55; DB 2; Length 105;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10

|||||||:|

Db 38 GYTFTNYGMN 47

RESULT 7

S26325
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
C/Accession: S26325

R/Starck, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ei

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <STA>

A/Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696F; EMBL:X59210; NID:g52080; PID:g

C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;5-88/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 55; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGIN 10
||| ||||| :
Db 16 GYFTNYGMN 25

RESULT 8

Ig heavy chain V region (M-T408) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19968
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <WEI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696A; EMBL:X65089
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;10-93/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 55; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGIN 10
||| ||||| :
Db 21 GYFTNYGMN 30

RESULT 9

Ig heavy chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19965
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19965
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <WEI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI0000176968; EMBL:X65088
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;8-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 55; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGIN 10
||| ||||| :
Db 19 GYFTNYGMN 28

RESULT 10

Ig heavy chain V region (M-T406) - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19967
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19967
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <WEI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI0000176969; EMBL:X65090
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;12-95/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 55; DB 2; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGIN 10
||| ||||| :
Db 23 GYFTNYGMN 32

RESULT 11

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles
A;Reference number: A53285; MUID:92017897; PMID:1922102
A;Accession: A53285
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-119 <SAW>
A;Cross-references: UNIPARC:UPI000011D0A7; GB:D12736; NID:g220595; PIDN:BA02228.1; PID: A53285
A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:P:63299)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 55; DB 2; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGIN 10
||| ||||| :
Db 26 GYFTNYGMN 35

RESULT 12

L6 mAb heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B42848; S33903
R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffi, J. Biol. Chem. 267, 15552-15558, 1992
A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and characterization
A;Reference number: A42848; MUID:92348410; PMID:1639794
A;Accession: B42848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120 <FEI>
A;Cross-references: UNIPARC:UPI0000115333; GB:M90690; NID:g195065; PIDN:AAA38146.1; PID: B42848
A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P:109961)
A;Accession: S33903
A;Status: preliminary
A;Molecule type: mRNA

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 53.3962 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-14
Perfect score: 58
Sequence: 1 GYTFNYGIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	91.4	120	1	P01747 mus musculus
2	53	91.4	140	1	HV03 MOUSE
3	50	86.2	241	2	Q21A6 MOUSE
4	50	86.2	475	2	Q5PQ51 RAT
5	47	81.0	486	2	Q5HZY6 MOUSE
6	46	79.3	117	1	HV52 MOUSE
7	46	79.3	458	2	Q5BJZ2 RAT
8	46	79.3	463	2	Q99LC4 MOUSE
9	45	77.6	125	2	Q6PIL0 HUMAN
10	45	77.6	140	2	Q65ZL3 9MURI
11	45	77.6	233	2	Q4ZGV0 9BACT
12	44	75.9	121	1	HV01 MOUSE
13	44	75.9	468	2	Q569W9 MOUSE
14	44	75.9	473	2	Q9DBL4 MOUSE
15	44	75.9	590	2	Q4V9V8 MOUSE
16	43	74.1	220	2	Q6X2N6 9BACT
17	43	74.1	220	2	Q6X2P6 uncultured
18	43	74.1	220	2	Q6X2P9 9BACT
19	43	74.1	220	2	Q8RT26 9BACT
20	43	74.1	220	2	Q9AP60 uncultured
21	43	74.1	220	2	Q9AP61 uncultured
22	43	74.1	220	2	Q9AP62 9BACT
23	43	74.1	220	2	Q9AP63 uncultured
24	43	74.1	220	2	Q6X2Q0 9BACT
25	43	74.1	220	2	Q6X2P0 9BACT
26	43	74.1	220	2	Q6X2N9 9BACT
27	43	74.1	233	2	Q4ZGQ6 9BACT
28	43	74.1	233	2	Q4ZGQ7 9BACT
29	43	74.1	233	2	Q4ZGR1 9BACT
30	43	74.1	233	2	Q4ZGR9 9BACT
31	43	74.1	233	2	Q4ZGS0 9BACT

32	43	74.1	233	2	Q4ZGS4 9BACT
33	43	74.1	233	2	Q4ZGT7 9BACT
34	43	74.1	233	2	Q4ZGV3 9BACT
35	43	74.1	447	2	Q5CJAL CRYHO
36	43	74.1	449	2	Q5CXK4 CRYPV
37	42	72.4	117	1	HV59 MOUSE
38	42	72.4	121	1	HV3J HUMAN
39	42	72.4	159	2	Q96QSO HUMAN
40	42	72.4	220	2	Q6X2P4 9BACT
41	42	72.4	220	2	Q6X2M7 9BACT
42	42	72.4	220	2	Q6VUY1 9BACT
43	42	72.4	224	2	Q5D3G1 9BACT
44	42	72.4	224	2	Q5D3G4 9BACT
45	42	72.4	224	2	Q5D3G6 9BACT

Q4zgs4 unidentified
Q4zgt7 unidentified
Q4zgv3 unidentified
Q5cjal cryptospori
Q5cxk4 cryptospori
P18530 mus musculus
P01771 homo sapien
Q96qso homo sapien
Q6x2p4 uncultured
Q6x2m7 uncultured
Q6vuy1 uncultured
Q5d3g1 uncultured
Q5d3g4 uncultured
Q5d3g6 uncultured

ALIGNMENTS

RESULT 1

ID	HV03 MOUSE	STANDARD;	PRT;	120 AA.
AC	P01747;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DB	IG heavy chain V region 36-65.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
EN	[1]			
RP	NUCLEOTIDE SEQUENCE			
RX	MEDLINE=83131846; PubMed=6186498;			
RA	Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,			
RA	Marshak-Rothstein A.;			
RT	"The genetic basis of antibody production: the dominant anti-arsonate			
RT	idiotype response of the strain A mouse.";			
RL	Eur. J. Immunol. 12:1023-1032(1982).			
[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.			
RX	MEDLINE=21528949; PubMed=11673524;			
RA	Parhami-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;			
RT	"Structural analysis of mutants of high-affinity and low-affinity p-			
RT	azophenylarsonate-specific antibodies generated by alanine scanning of			
RL	heavy chain complementarity-determining region 2.";			
CC	J. Immunol. 167:5129-5135(2001).			
CC	-1- MISCELLANEOUS: From analysis of the sizes of several other			
CC	differentiated genes that hybridize to this one, the authors			
CC	conclude that all of these V regions have rearranged to the same J			
CC	segment, JH2.			
CC	-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	PIR; A94264; HVM5G7.			
DR	PDB; 1JFQ; X-ray; H=1-120.			
DR	Ensembl; ENSMUSG0000021155; Mus musculus.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
DR	3D-structure; Hybridoma; Immunoglobulin domain;			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 111			
FT	NON TER 120 120			
FT	SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;			
SQ				

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Query Match          91.4%; Score 53; DB 1; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 25 GYTFTSYGIN 34

RESULT 2
HV02 MOUSE          STANDARD; PRT; 140 AA.
ID HV02 MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Eteses P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00493; AAA38128.1; -; mRNA.
CC HSSP; P01747; 1JFQ.
CC SMR; P01746; 20-140.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PSS00835; IG_LIKE; 1.
CC HYBRIDOMA; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 Ig heavy chain V region 93G7.
FT DOMAIN 20 139 Ig-like.
FT NON_TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C88 CRC64;

Query Match          91.4%; Score 53; DB 1; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 45 GYTFTSYGIN 54

RESULT 3
Q921A6 MOUSE
ID Q921A6 MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR Ensemble; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 2_v.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 241 241
FT SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match          86.2%; Score 50; DB 2; Length 241;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 26 GYTFTSYGIN 35

RESULT 4
QSPQ51 RAT
ID QSPQ51 RAT PRELIMINARY; PRT; 475 AA.
AC QSPQ51;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DB IgA protein.
GN Name-IgA;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
```

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

```

FT DISULPID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 79.3%; Score 46; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTPTNYGIN 10
Db 45 GYFTPTNYDIN 54

RESULT 7
Q5BJZ2 RAT PRELIMINARY; PRT; 458 AA.
AC Q5BJZ2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AAH91272.1; -, mRNA.
DR SMR; Q5BJZ2; 21-454.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

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Query Match 79.3%; Score 46; DB 2; Length 458;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTPTNYGIN 10
Db 45 GYFTPTNYDIN 54

RESULT 8
Q99LC4 MOUSE PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-4 protein.
GN Name=Igh-4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -, mRNA.
DR PIR; B45837; B45837.
DR HSPSP; P01869; ICL7.
DR SMR; Q99LC4; 21-459.
DR MGI; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Vertebrata); IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0050766; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IDA.

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Tue Apr 25 08:25:42 2006

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;

Query Match 79.3%; Score 46; DB 2; Length 463;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFNYGIN 10
Db 45 GYTFYGVGS 54

RESULT 9
Q6PIL0_HUMAN
ID Q6PIL0_HUMAN PRELIMINARY; PRT; 125 AA.
AC Q6PIL0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHV7-81 protein.
GN Name=IGHV7-81;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP TISSUE=Lymph;
RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan J., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Patney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032733; AAH32733.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6PIL0; 20-117.
DR HGNC; HGNC:5669; IGHV7-81.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 125 AA; 13913 MW; B76CE434F5A69788 CRC64;

Query Match 77.6%; Score 45; DB 2; Length 125;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFNYGIN 10
Db 45 GYTFYGVGS 54

us-10-764-428-14.rup
Best Local Similarity 70.0%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFNYGIN 10
Db 45 GYTFYGVGS 54

RESULT 10
Q65ZL3_9MURI
ID Q65ZL3_9MURI PRELIMINARY; PRT; 140 AA.
AC Q65ZL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tg10H (Fragment).
GN Name=Tg10H;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;
RA Noel D., Bernardi T., Navarro-Teulon I., Marin M., Martinetto J.P.,
Ducancel P., Mani J.C., Pau B., Piechaczyk M., Biard-Piechaczyk M.;
RT "Analysis of the individual contributions of immunoglobulin heavy and
light chains to the binding of antigen using cell transfection and
plasmon resonance analysis."
RL J. Immunol. Methods 193:177-187(1996).
DR EMBL; S82492; AAB37434.2; -; mRNA.
DR SMR; Q65ZL3; 20-140.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 1.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 140
SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965F43 CRC64;

Query Match 77.6%; Score 45; DB 2; Length 140;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFNYGI 9
Db 45 GYTFYGYL 53

RESULT 11
Q4ZGV0_9BACT
ID Q4ZGV0_9BACT PRELIMINARY; PRT; 233 AA.
AC Q4ZGV0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS unidentified bacterium.
OC Bacteria; environmental samples.
OC NCBI_TaxID=2338;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dambreville C., Philippot L.;
RT "Structure and activity of the denitrifying community in a maize
planted soil fertilized with pig compost or ammonium nitrate."
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ010807; AAY30755.1; -; Genomic_DNA.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.

```

DR ProDom; PD000131; Copper CUA; 1.
 DR PROSITE; PS50857; COX2_CUA; 1.
 FT NON_TER 1 233
 FT NON_TER 233 233
 SQ SEQUENCE 233 AA; 26271 MW; 194F23F11497D008 CRC64;

Query Match 77.6%; Score 45; DB 2; Length 233;
 Best Local Similarity 70.0%; Pred. No. 8.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
 ||| |||||:
 Db 190 GYCITNYGVN 199

RESULT 12

ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable region
 of immunoglobulin heavy chain MPC11.";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 RN [2]
 RP ERRATUM, AND SEQUENCE REVISION.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -1- MISCELLANEOUS: This sequence was translated from an mRNA isolated
 from a myeloma that secretes IgG2b.
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR PIR; A93708; GVMS11.
 DR HSP; P01751; INQB.
 DR SMR; P01745; 1-121.
 DR Ensembl; ENSMUSG00000062635; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region.
 FT DOMAIN 1 112
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 75.9%; Score 44; DB 1; Length 121;
 Best Local Similarity 88.9%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTNYGI 9
 |||||:
 Db 26 GYFTNYWI 34

RESULT 13

Q569W9_MOUSE

ID Q569W9_MOUSE PRELIMINARY; PRT; 468 AA.
 AC Q569W9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH 11;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH 11;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC092271; AAH92271.1; -; mRNA.
 DR SMR; Q569W9; 20-464.
 DR MGI; MGI:96443; Igh-1a.
 DR GO; GO:0003923; F-antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;

Query Match 75.9%; Score 44; DB 2; Length 468;
 Best Local Similarity 80.0%; Pred. No. 25;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
 |||||:
 Db 45 GYFTSYIN 54

RESULT 14

Q9D8L4_MOUSE

ID Q9D8L4_MOUSE PRELIMINARY; PRT; 473 AA.

AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
 DE library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
 DE chain of IgM), full insert sequence.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guatinchich S., Hill D., Hofmann H., Hume D.A., Kaniwa M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Wombert P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RC The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RC MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiranoto K., Hiraoka T., Hori F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007918; BAB25349.1; -; mRNA.
 DR PIR; PH1165; PH1165.
 DR PIR; S19966; S19966.
 DR PIR; S26746; S26746.
 DR HSP; P01864; L80G.
 DR SMR; Q9D8L4; 20-469.
 DR ENSEMBL; ENSMUSG00000054328; Mus musculus.
 DR MGI; MGI:96443; Igh-1a.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0005771; C:multivesicular body; IDA.
 DR GO; GO:0003823; P:antigen binding; IDA.
 DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
 DR GO; GO:0030333; P:antigen processing; IDA.
 DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
 DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
 DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
 DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
 DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
 DR GO; GO:0050778; P:positive regulation of immune response; IDA.
 DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
 DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
 DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.
 DR GO; GO:0030182; P:regulation of proteolysis and peptidolysis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 473 AA; 51699 MW; 9DBD57A514475FBB CRC64;

Query Match 75.9%; Score 44; DB 2; Length 473;
 Best Local Similarity 80.0%; Pred. NO. 25;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYTFNTNGIN 10
 Db 45 GYTFNTNGIN 54

RESULT 15

Q4V9V8 MOUSE
 ID Q4V9V8_MOUSE PRELIMINARY; PRT; 590 AA.
 AC Q4V9V8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC096667; AAH96667.1; -; mRNA.
DR MGI; MGI:96448; Igh-6.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;

Query Match 75.9%; Score 44; DB 2; Length 590;
Best Local Similarity 80.0%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
Db 45 GYFTDYIN 54

Search completed: April 25, 2006, 06:24:37
Job time : 55.3962 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 13.4906 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-14

Perfect score: 58

Sequence: 1 GYFTYNGIN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	118	2	US-08-908-469-110
2	58	100.0	118	2	US-08-908-469-114
3	55	94.8	10	2	US-08-908-469-1
4	55	94.8	92	2	US-08-783-853A-84
5	55	94.8	92	2	US-09-344-050-84
6	55	94.8	112	2	US-08-783-853A-20
7	55	94.8	112	2	US-09-344-050-20
8	55	94.8	118	1	US-08-425-336-124
9	55	94.8	118	1	US-08-425-336-126
10	55	94.8	118	1	US-08-488-113B-124
11	55	94.8	118	1	US-08-488-113B-126
12	55	94.8	118	1	US-08-477-484B-124
13	55	94.8	118	1	US-08-477-484B-126
14	55	94.8	118	1	US-08-107-669D-28
15	55	94.8	118	1	US-08-107-669D-29
16	55	94.8	118	1	US-08-107-669D-66
17	55	94.8	118	1	US-08-107-669D-67
18	55	94.8	118	1	US-08-472-788A-28
19	55	94.8	118	1	US-08-472-788A-29
20	55	94.8	118	1	US-08-472-788A-88
21	55	94.8	118	1	US-08-472-788A-99
22	55	94.8	118	1	US-08-477-531B-28
23	55	94.8	118	1	US-08-477-531B-29
24	55	94.8	118	1	US-08-477-531B-66
25	55	94.8	118	1	US-08-477-531B-67
26	55	94.8	118	1	US-08-646-360-124
27	55	94.8	118	1	US-08-646-360-126

Sequence 28, Appl
Sequence 29, Appl
Sequence 88, Appl
Sequence 89, Appl
Sequence 124, App
Sequence 126, App
Sequence 124, App
Sequence 126, App
Sequence 126, App
Sequence 124, App
Sequence 126, App
Sequence 96, Appl
Sequence 124, App
Sequence 126, App
Sequence 104, App
Sequence 108, App
Sequence 9, Appl
Sequence 78, Appl

28 28 94.8 118 1 US-08-082-842A-28
29 28 94.8 118 1 US-08-082-842A-29
30 28 94.8 118 1 US-08-082-842A-88
31 28 94.8 118 1 US-08-082-842A-89
32 28 94.8 118 2 US-08-839-765-124
33 28 94.8 118 2 US-08-839-765-126
34 28 94.8 118 2 US-09-136-389-124
35 28 94.8 118 2 US-09-136-389-126
36 28 94.8 118 2 US-09-610-838-124
37 28 94.8 118 2 US-09-610-838-126
38 28 94.8 118 2 US-09-440-781-96
39 28 94.8 118 2 US-09-711-485-124
40 28 94.8 118 2 US-09-711-485-126
41 28 94.8 118 2 US-08-908-469-104
42 28 94.8 118 2 US-08-908-469-106
43 28 94.8 118 2 US-08-908-469-108
44 28 94.8 118 2 US-10-368-883-9
45 28 94.8 119 2 US-08-933-983-78

ALIGNMENTS

RESULT 1

US-08-908-469-110
Sequence 110, Application US/08908469
Patent No. 6884879

GENERAL INFORMATION:

APPLICANT: Baca, Manuel
Wellis, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 110:

US-08-908-469-110

Query Match 100.0%; Score 58; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
|||||
Db 26 GYTFTNYGIN 35

RESULT 2

US-08-908-469-114
; Sequence 114, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: F1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-08-908-469-114

Query Match 100.0%; Score 58; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
|||||
Db 26 GYTFTNYGIN 35

RESULT 3

US-08-908-469-1
; Sequence 1, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: F1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-908-469-1

Query Match 94.8%; Score 55; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
|||||
Db 1 GYTFTNYGMN 10

RESULT 4

US-08-783-853A-84
; Sequence 84, Application US/08783853A
; Patent No. 6005091
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,853A
; FILING DATE: 16-JAN-1997

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvestre, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-20

Query Match 94.8%; Score 55; DB 2; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 23 GYTFTNYGMN 32

RESULT 7

US-09-344-050-20
; Sequence 20, Application US/09344050
; Patent No. 6391299
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,050
; FILING DATE: 24-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/783,853
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-344-050-20

Query Match 94.8%; Score 55; DB 2; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 23 GYTFTNYGMN 32

RESULT 8

US-08-425-336-124
; Sequence 124, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-8402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-124

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
DB 26 GYTFTNYGMN 35

RESULT 9

US-08-425-336-126

```

; Sequence 126, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-126

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYFTNYGIN 10
Db 26 GYFTNYGMN 35

RESULT 10
US-08-488-113B-124
; Sequence 124, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:

; Sequence 126, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-124

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYFTNYGIN 10
Db 26 GYFTNYGMN 35

RESULT 11
US-08-488-113B-126
; Sequence 126, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-126

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
Db 26 GYFTNYGMN 35

RESULT 12

US-08-477-484B-124
Sequence 124, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-124

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
Db 26 GYFTNYGMN 35

RESULT 13

US-08-477-484B-126
Sequence 126, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336

;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA: US 08/064,691
;; APPLICATION NUMBER: 12-MAY-1993
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 126:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-126

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
Db 26 GYTFTNYGMN 35

RESULT 14
US-08-107-669D-28
; Sequence 28, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202/371-2600
;; TELEFAX: 202/371-2540
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-107-669D-28

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
Db 26 GYTFTNYGMN 35

RESULT 15
US-08-107-669D-29
; Sequence 29, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-29

Query Match 94.8%; Score 55; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
Db 26 GYTFTNYGMN 35

Search completed: April 25, 2006, 06:28:38
Job time : 13.4906 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:58:17 ; Search time 43.5849 Seconds
(without alignments)
95.866 Million cell updates/sec

Title: US-10-764-428-14
Perfect score: 58
Sequence: 1 GYTFNYGIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	5	US-10-764-428-14
2	58	100.0	118	3	US-09-056-160B-110
3	58	100.0	118	3	US-09-056-160B-114
4	58	100.0	118	4	US-10-234-671-108
5	58	100.0	118	4	US-10-234-671-112
6	58	100.0	118	5	US-10-683-043-11
7	58	100.0	118	5	US-10-974-591-108
8	58	100.0	118	5	US-10-974-591-112
9	58	100.0	479	5	US-10-697-995-12
10	58	100.0	670	5	US-10-764-428-5
11	58	100.0	670	5	US-10-764-428-9
12	58	100.0	670	5	US-10-764-428-11
13	58	100.0	670	5	US-10-764-428-27
14	57	98.3	120	5	US-10-706-852-2
15	57	98.3	120	5	US-10-706-852-6
16	57	98.3	120	5	US-10-706-852-10
17	55	94.8	10	3	US-09-056-160B-1
18	55	94.8	10	4	US-10-234-671-1
19	55	94.8	10	4	US-10-018-245A-1
20	55	94.8	10	4	US-10-723-434-112
21	55	94.8	10	4	US-10-723-434-116
22	55	94.8	10	5	US-10-974-591-1
23	55	94.8	67	4	US-10-243-130-19
24	55	94.8	70	4	US-10-243-130-17
25	55	94.8	70	4	US-10-243-130-18
26	55	94.8	70	5	US-10-901-650-17
27	55	94.8	70	5	US-10-901-650-18

28	55	94.8	70	5	US-10-901-650-19	Sequence 19, Appl
29	55	94.8	92	3	US-09-965-099-84	Sequence 84, Appl
30	55	94.8	92	4	US-10-051-852-84	Sequence 84, Appl
31	55	94.8	92	4	US-10-430-176-84	Sequence 84, Appl
32	55	94.8	92	4	US-10-681-421-84	Sequence 84, Appl
33	55	94.8	112	3	US-09-965-099-20	Sequence 20, Appl
34	55	94.8	112	4	US-10-051-852-20	Sequence 20, Appl
35	55	94.8	112	4	US-10-430-176-20	Sequence 20, Appl
36	55	94.8	112	4	US-10-681-421-20	Sequence 20, Appl
37	55	94.8	113	5	US-10-830-899-50	Sequence 50, Appl
38	55	94.8	113	5	US-10-830-899-57	Sequence 57, Appl
39	55	94.8	113	5	US-10-861-662-50	Sequence 57, Appl
40	55	94.8	113	5	US-10-861-662-57	Sequence 57, Appl
41	55	94.8	116	3	US-09-971-543-8	Sequence 8, Appl
42	55	94.8	116	3	US-09-971-543-9	Sequence 9, Appl
43	55	94.8	116	3	US-09-971-543-10	Sequence 10, Appl
44	55	94.8	116	4	US-10-138-727A-2	Sequence 2, Appl
45	55	94.8	116	4	US-10-138-727A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-764-428-14
; Sequence 14, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION: Laura
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; FILE REFERENCE: 11669,120USU1
; CURRENT APPLICATION NUMBER: US/10/764,428
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HVR1 residues 26-35
US-10-764-428-14

Query Match 100.0%; Score 58; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFNYGIN 10
| | | | | | | | | |
Db 1 GYTFNYGIN 10

RESULT 2
US-09-056-160B-110
; Sequence 110, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, Manuel
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

```
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet B.
; REGISTRATION NUMBER: 28,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-160B-110

Query Match 100.0%; Score 58; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
Db 26 GYFTFTNYGIN 35

RESULT 4
US-10-234-671-108
; Sequence 108, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION NUMBER: 09/056160
; FILING DATE: 06-Apr-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-Apr-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-234-671-108

Query Match 100.0%; Score 58; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
```


Qy 1 GYFTNYGIN 10
| | | | | | | |
Db 26 GYFTNYGIN 35

RESULT 8

US-10-974-591-112
; Sequence 112, Application US/10974591
; Publication No. US20050112126A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/974,591

; FILING DATE: 26-Oct-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/723752

; FILING DATE: 27-NOV-2000

; APPLICATION NUMBER: 08/908469

; FILING DATE: 06-AUG-1997

; APPLICATION NUMBER: 08/833504

; FILING DATE: 07-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Cui, Steven X.

; REGISTRATION NUMBER: 44,637

; REFERENCE/DOCKET NUMBER: P1093P1D1C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 112:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 118 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-974-591-112

Query Match 100.0%; Score 58; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
| | | | | | | |
Db 26 GYFTNYGIN 35

RESULT 9

US-10-697-995-12

; Sequence 12, Application US/10697995

; Publication No. US20050048572A1

; GENERAL INFORMATION:

; APPLICANT: Reilly, Dorothea

; APPLICANT: Yansura, Daniel G.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

; FILE REFERENCE: 11669.195USU1
; CURRENT APPLICATION NUMBER: US/10/697,995
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/422,952
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 12
; LENGTH: 479

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Anti-VEGF heavy chain

US-10-697-995-12

Query Match 100.0%; Score 58; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
| | | | | | | |

Db 49 GYFTNYGIN 58
| | | | | | | |

RESULT 10

US-10-764-428-5

; Sequence 5, Application US/10764428

; Publication No. US20040229310A1

; GENERAL INFORMATION:

; APPLICANT: Simmons, Laura

; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING

; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL

; TITLE OF INVENTION: CULTURE

; FILE REFERENCE: 11669.120USU1

; CURRENT APPLICATION NUMBER: US/10/764,428

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US 60/442,484

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 670

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The first 214 amino acids are the light chain followed by the

; OTHER INFORMATION: heavy chain beginning at position 215 (E).

US-10-764-428-5

Query Match 100.0%; Score 58; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
| | | | | | | |

Db 240 GYFTNYGIN 249
| | | | | | | |

RESULT 11

US-10-764-428-9

; Sequence 9, Application US/10764428

; Publication No. US20040229310A1

; GENERAL INFORMATION:

; APPLICANT: Simmons, Laura

; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING

; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL

; TITLE OF INVENTION: CULTURE

; FILE REFERENCE: 11669.120USU1

; CURRENT APPLICATION NUMBER: US/10/764,428

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US 60/442,484

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 9
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at
; OTHER INFORMATION: residue 215 (Q)
US-10-764-428-9

Query Match      100.0%; Score 58; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFNYGIN 10
      |||||
Db      240 GYTFNYGIN 249

RESULT 12
US-10-764-428-11
; Sequence 11, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; TITLE OF INVENTION: CULTURE
; FILE REFERENCE: 11669.120USU1
; CURRENT APPLICATION NUMBER: US/10/764,428
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at
; OTHER INFORMATION: residue 215 (Q)
US-10-764-428-11

Query Match      100.0%; Score 58; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFNYGIN 10
      |||||
Db      240 GYTFNYGIN 249

RESULT 13
US-10-764-428-27
; Sequence 27, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; TITLE OF INVENTION: CULTURE
; FILE REFERENCE: 11669.120USU1
; CURRENT APPLICATION NUMBER: US/10/764,428
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at
; OTHER INFORMATION: residue 215 (Q)
US-10-764-428-27

Query Match      100.0%; Score 58; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFNYGIN 10
      |||||
Db      240 GYTFNYGIN 249

RESULT 14
US-10-706-852-2
; Sequence 2, Application US/10706852
; Publication No. US20040219203A1
; GENERAL INFORMATION:
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: LUNDBERG, BO B.
; TITLE OF INVENTION: ANTI-CD74 IMMUNOCONJUGATES AND METHODS
; FILE REFERENCE: 40923-0079US5
; CURRENT APPLICATION NUMBER: US/10/706,852
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/314,330
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/965,796
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/307,816
; PRIOR FILING DATE: 1999-05-10
; PRIOR APPLICATION NUMBER: 10/350,096
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/590,284
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 10/377,122
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/360,259
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/478,830
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-706-852-2

Query Match      98.3%; Score 57; DB 5; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFNYGIN 10
      |||||
Db      26 GYTFNYGIN 35

RESULT 15
US-10-706-852-6
; Sequence 6, Application US/10706852
; Publication No. US20040219203A1
; GENERAL INFORMATION:
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: LUNDBERG, BO B.
; TITLE OF INVENTION: ANTI-CD74 IMMUNOCONJUGATES AND METHODS
; FILE REFERENCE: 40923-0079US5
; CURRENT APPLICATION NUMBER: US/10/706,852
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/314,330
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; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/965,796
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/307,816
; PRIOR FILING DATE: 1999-05-10
; PRIOR APPLICATION NUMBER: 10/350,096
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/590,284
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 10/377,122
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/360,259
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/478,830
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric cLL1VH sequence
US-10-706-852-6

Query Match      98.3%; Score 57; DB 5; Length 120;
Best Local Similarity 90.0%; Pred.No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTNYGIN 10
      |||||:|
Db      26 GYFTNYGVN 35

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Search completed: April 25, 2006, 07:08:46
Job time : 44.5849 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 6.41509 Seconds

(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-14

Perfect score: 58

Sequence: 1 GYTFNYGIN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PTC NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	118	6	US-10-648-816-11
2	55	94.8	92	7	US-11-240-195-84
3	55	94.8	112	7	US-11-240-195-20
4	55	94.8	116	7	US-11-174-186-2
5	55	94.8	116	7	US-11-174-186-4
6	55	94.8	116	7	US-11-174-186-6
7	55	94.8	116	7	US-11-174-186-17
8	55	94.8	116	7	US-11-174-186-18
9	55	94.8	116	7	US-11-174-186-19
10	55	94.8	116	7	US-11-174-186-20
11	55	94.8	116	7	US-11-174-186-21
12	55	94.8	116	7	US-11-174-186-22
13	55	94.8	116	7	US-11-174-186-23
14	55	94.8	116	7	US-11-174-186-24
15	55	94.8	116	7	US-11-174-186-25
16	55	94.8	116	7	US-11-174-186-26
17	55	94.8	117	7	US-11-174-186-35
18	55	94.8	117	7	US-11-037-199-32
19	55	94.8	118	6	US-10-648-816-9
20	55	94.8	118	6	US-10-648-816-14
21	55	94.8	121	6	US-10-648-816-15
22	55	94.8	121	7	US-11-240-195-7
23	55	94.8	121	7	US-11-240-195-31
24	55	94.8	121	7	US-11-240-195-52
25	55	94.8	121	7	US-11-240-195-111

ALIGNMENTS

RESULT 1

US-10-648-816-11 123 7 US-11-240-195-109
 ; Sequence 11, Application US/10648816
 ; Publication No. US2005024405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Bruggen, Nicholas
 ; APPLICANT: Ferrara, Napoleone
 ; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
 ; TITLE OF INVENTION: and Uses Thereof
 ; FILE REFERENCE: P1717D1
 ; CURRENT APPLICATION NUMBER: US/10/648,816
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: US/09/718,694
 ; PRIOR FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: US 09/218,481
 ; PRIOR FILING DATE: 1998-12-22
 ; NUMBER OF SEQ ID NOS: 16
 ; SEQ ID NO 11
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-648-816-11

Query Match 100.0%; Score 58; DB 6; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFNYGIN 10
 |||||
 Db 26 GYTFNYGIN 35

RESULT 2

US-11-240-195-84
 ; Sequence 84, Application US/11240195
 ; Publication No. US20060057140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Feuerstein, Gloria Z.
 ; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
 ; TITLE OF INVENTION: OF THROMBOSIS
 ; FILE REFERENCE: P50816-1
 ; CURRENT APPLICATION NUMBER: US/11/240,195
 ; CURRENT FILING DATE: 2005-09-30
 ; PRIOR APPLICATION NUMBER: US/10/430,176
 ; PRIOR FILING DATE: 2003-05-05
 ; PRIOR APPLICATION NUMBER: 09/817,960
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/359,202

Sequence 109, Appl
 Sequence 8, Appl
 Sequence 10, Appl
 Sequence 89, Appl
 Sequence 41, Appl
 Sequence 1885, Ap
 Sequence 2124, Ap
 Sequence 2126, Ap
 Sequence 1885, Ap
 Sequence 2124, Ap
 Sequence 2126, Ap
 Sequence 1008, Ap
 Sequence 1008, Ap
 Sequence 1897, Ap
 Sequence 1897, Ap
 Sequence 1897, Ap
 Sequence 1897, Ap
 Sequence 1530, Ap

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; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 60/095,714
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-84

Query Match          94.8%; Score 55; DB 7; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
Db 3 GYTFTNYGMN 12
|||||||:|

RESULT 3
US-11-240-195-20
; Sequence 20, Application US/11240195
; Publication No. US20060057140A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; FILE REFERENCE: PS0816-1
; CURRENT APPLICATION NUMBER: US/11/240,195
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/10/430,176
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 09/817,960
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/359,202
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 60/095,714
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-20

Query Match          94.8%; Score 55; DB 7; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
Db 3 GYTFTNYGMN 12
|||||||:|

US-11-174-186-2
; Sequence 4, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH mouse
US-11-174-186-2

Query Match          94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
Db 26 GYTFTNYGMN 35
|||||||:|

RESULT 5
US-11-174-186-4
; Sequence 4, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable heavy chain sequence in the EpCAM antibody
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
```



```
OTHER INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
FEATURE:
NAME/KEY: misc feature
LOCATION: (17)..(17)
OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
FEATURE:
NAME/KEY: misc feature
LOCATION: (38)..(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
FEATURE:
NAME/KEY: misc feature
LOCATION: (40)..(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
FEATURE:
NAME/KEY: misc feature
LOCATION: (43)..(43)
OTHER INFORMATION: wherein Xaa at position 43 is a lysine or a glutamine
FEATURE:
NAME/KEY: misc feature
LOCATION: (46)..(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (63)..(63)
OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
FEATURE:
NAME/KEY: misc feature
LOCATION: (65)..(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
FEATURE:
NAME/KEY: misc feature
LOCATION: (69)..(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
FEATURE:
NAME/KEY: misc feature
LOCATION: (70)..(70)
OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
FEATURE:
NAME/KEY: misc feature
LOCATION: (71)..(71)
OTHER INFORMATION: wherein Xaa at position 71 is a serine or a threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (72)..(72)
OTHER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
FEATURE:
NAME/KEY: misc feature
LOCATION: (73)..(73)
OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (76)..(76)
OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (79)..(79)
OTHER INFORMATION: wherein Xaa at position 79 is an alanine or a leucine
FEATURE:
NAME/KEY: misc feature
LOCATION: (80)..(80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
FEATURE:
NAME/KEY: misc feature
LOCATION: (83)..(83)
OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
FEATURE:
NAME/KEY: misc feature
LOCATION: (84)..(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
```

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FEATURE:
NAME/KEY: misc feature
LOCATION: (85)..(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
FEATURE:
NAME/KEY: misc feature
LOCATION: (88)..(88)
OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or a
OTHER INFORMATION: serine
FEATURE:
NAME/KEY: misc feature
LOCATION: (91)..(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (93)..(93)
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
FEATURE:
NAME/KEY: misc feature
LOCATION: (100)..(100)
OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
FEATURE:
NAME/KEY: misc feature
LOCATION: (108)..(108)
OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
FEATURE:
NAME/KEY: misc feature
LOCATION: (111)..(111)
OTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine
US-11-174-186-4
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Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GYTFTNYGIN 10
Db 26 GYTFTNYGMN 35
|||||:|
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RESULT 6
US-11-174-186-6
; Sequence 6, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: heavy sequence consensus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
```

; OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (38)..(38)
; OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (63)..(63)
; OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)..(68)
; OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (76)..(76)
; OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)..(80)
; OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (83)..(83)
; OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (84)..(84)
; OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (85)..(85)
; OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)..(88)
; OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or a
; OTHER INFORMATION: serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (93)..(93)

; OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108)..(108)
; OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
; US-11-174-186-6

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
Db 26 GYTFTNYGMN 35
|||||||:

RESULT 7

US-11-174-186-17
; Sequence 17, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH6 heavy chain
; US-11-174-186-17

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTNYGIN 10
Db 26 GYTFTNYGMN 35
|||||||:

RESULT 8

US-11-174-186-18
; Sequence 18, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH7 heavy chain
; US-11-174-186-18

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
DB 26 GYTFTNYGMN 35

RESULT 9
US-11-174-186-19
; Sequence 19, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH2.5 heavy chain
US-11-174-186-19

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
DB 26 GYTFTNYGMN 35

RESULT 10
US-11-174-186-20
; Sequence 20, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH veneered
US-11-174-186-20

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
DB 26 GYTFTNYGMN 35

RESULT 11

US-11-174-186-21
; Sequence 21, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH1
US-11-174-186-21

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
DB 26 GYTFTNYGMN 35

RESULT 12

US-11-174-186-22
; Sequence 22, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTNYGIN 10
||| ||||| :
DB 26 GYTFTNYGMN 35

RESULT 13

US-11-174-186-23
; Sequence 23, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH3
US-11-174-186-23

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
|||||||:
Db 26 GYFTFTNYGMN 35

RESULT 14
US-11-174-186-24
; Sequence 24, Application US/11/174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS- deimmunized VH4
US-11-174-186-24

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
|||||||:
Db 26 GYFTFTNYGMN 35

RESULT 15
US-11-174-186-25
; Sequence 25, Application US/11/174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01

; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match 94.8%; Score 55; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
|||||||:
Db 26 GYFTFTNYGMN 35

Search completed: April 25, 2006, 07:10:01
Job time : 7.58176 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 53.3962 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-18

Perfect score: 62

Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	10	2 AAW70662	Aaw70662 Fab-phage
2	62	100.0	10	2 AAW70698	Aaw70698 Anti-VEGF
3	62	100.0	10	5 ABP61231	Abp61231 Anti-VEGF
4	62	100.0	10	5 ABP61267	Abp61267 Humanised
5	62	100.0	10	8 ADQ90714	Adq90714 Anti-VEGF
6	62	100.0	117	7 ADF09953	Adf09953 Antibody
7	62	100.0	117	7 ADF10058	Adf10058 VEGF anti
8	62	100.0	118	2 AAW70686	Aaw70686 Anti-VEGF
9	62	100.0	118	2 AAW70688	Aaw70688 Anti-VEGF
10	62	100.0	118	2 AAW70682	Aaw70682 Anti-VEGF
11	62	100.0	118	3 AAB05900	Aab05900 F(ab)-12
12	62	100.0	118	3 AAB13382	Aab13382 Anti-VEGF
13	62	100.0	118	3 AAB13385	Aab13385 Anti-VEGF
14	62	100.0	118	3 AAB13384	Aab13384 Anti-VEGF
15	62	100.0	118	5 ABP61255	Abp61255 Humanised
16	62	100.0	118	5 ABP61257	Abp61257 Humanised
17	62	100.0	118	5 ABP61251	Abp61251 Humanised
18	62	100.0	121	3 AAB05902	Aab05902 F(ab)-12
19	62	100.0	121	3 AAB13391	Aab13391 Anti-VEGF
20	62	100.0	123	8 ADG31769	Adg31769 V(H) doma
21	62	100.0	123	9 AEA40494	Aea40494 Anti-VEGF
22	62	100.0	254	5 ABP51953	Abp51953 Plaamid p
23	62	100.0	476	5 ABB81110	Abb81110 Anti-VEGF
24	62	100.0	476	8 AD014129	Ad014129 Plaamid p

ALIGNMENTS

RESULT 1

AAW70662

ID AAW70662 standard; peptide; 10 AA.

XX AC AAW70662;

XX AC AAW70662;

DT 27-JAN-1999 (first entry)

XX DB Fab-phage library HL-265 anti-VEGF variant Y0243-1.

XX XX

Murine; humanised antibody; VEGF-induced angiogenesis; tumour;
anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
retinal disorder; age-related macular degeneration; diabetic retinopathy;
rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX OS Synthetic.

XX PN WO9845331-A2.

XX PN 15-OCT-1998.

XX PD 03-APR-1998; 98WO-US006604.

XX PF 07-APR-1997; 97US-008333504.

XX PR 06-AUG-1997; 97US-00908469.

XX XX (GETH) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX PI WPI; 1998-568337/48.

XX PT New humanised antibody with affinity for vascular endothelial growth

XX PT factor - for treatment of tumours, retinal disease and other angiogenic

XX PT states, also related nucleic acid, vectors and transformed cells.

XX XX Example 3; Page 74; 100pp; English.

XX CC AAW70662-67 represent murine anti-vascular endothelial growth factor

XX CC (anti-VEGF) antibody variants from Fab-phage library HL-265. The

XX CC sequences are used in the course of the invention to produce the

XX CC humanised anti-VEGF antibody of the invention. The humanised antibodies

XX CC are used to inhibit VEGF-induced angiogenesis, particularly for treating

XX CC or preventing tumours (of any type) and retinal disorders (e.g. age-

XX CC related macular degeneration or diabetic retinopathy). They can also be

XX CC used to treat other conditions that involve angiogenesis, e.g. rheumatoid

XX CC arthritis, psoriasis, atherosclerosis, Grave's disease, etc

Adq90730 Anti-VEGF
Adq90733 Anti-VEGF
Aea40565 Anti-VEGF
Aea40533 Anti-VEGF
Aaw70664 Fab-phage
Aaw70666 Fab-phage
Abp61233 Anti-VEGF
Abp61235 Anti-VEGF
Aaw70665 Fab-phage
Abp61234 Anti-VEGF
Aea40569 Anti-VEGF
Aea40573 Anti-VEGF
Aea17137 Human TNP
Aea40548 Anti-VEGF
Aea40544 Anti-VEGF
Adc26162 Anti-VEGF
Adc26158 Anti-VEGF
Adc26161 Anti-VEGF
Adc26163 Anti-VEGF
Aaw70667 Fab-phage
Abp61236 Anti-VEGF

25 62 100.0 476 8 ADQ90730
26 62 100.0 476 8 ADQ90733
27 59 95.2 10 9 AEA40565
28 59 95.2 123 9 AEA40533
29 58 93.5 10 2 AAW70664
30 58 93.5 10 2 AAW70666
31 58 93.5 10 5 ABP61233
32 58 93.5 10 5 ABP61235
33 55 88.7 10 2 AAW70665
34 55 88.7 10 5 ABP61234
35 55 88.7 10 9 AEA40569
36 55 88.7 10 9 AEA40573
37 55 88.7 117 9 AEA17137
38 55 88.7 123 9 AEA40548
39 55 88.7 123 9 AEA40544
40 55 88.7 231 7 ADC26162
41 55 88.7 231 7 ADC26158
42 55 88.7 234 7 ADC26161
43 55 88.7 234 7 ADC26163
44 54 87.1 10 2 AAW70667
45 54 87.1 10 5 ABP61236

```

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 62; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 2
AAW70698
ID AAW70698 standard; peptide; 10 AA.
XX AC AAW70698;
XX DT 27-JAN-1999 (first entry)
XX DE Anti-VEGF antibody heavy chain hypervariable region CDRH1.
XX KW Heavy chain hypervariable region; murine; humanised antibody;
XX KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX KW VEGF-induced angiogenesis; tumour; retinal disorder;
XX KW age-related macular degeneration; diabetic retinopathy;
XX KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9845331-A2.
XX PD 15-OCT-1998.
XX PF 03-APR-1998; 98WO-US006604.
XX PR 07-APR-1997; 97US-00833504.
XX PR 06-AUG-1997; 97US-00908469.
XX PA (GETH ) GENENTECH INC.
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI; 1998-568337/48.
XX PT New humanised antibody with affinity for vascular endothelial growth
XX factor - for treatment of tumours, retinal disease and other angiogenic
XX states, also related nucleic acid, vectors and transformed cells.
XX PS Claim 23; Page 81; 100pp; English.
XX CC The present sequence represents a heavy chain hypervariable region of the
XX CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The
XX CC sequence is used to construct the humanised anti-VEGF antibody of the
XX CC invention. The humanised antibodies are used to inhibit VEGF-induced
XX CC angiogenesis, particularly for treating or preventing tumours (of any
XX CC type) and retinal disorders (e.g. age-related macular degeneration or
XX CC diabetic retinopathy). They can also be used to treat other conditions
XX CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
XX CC atherosclerosis, Grave's disease, etc
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 62; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 3
ABP61231
ID ABP61231 standard; peptide; 10 AA.
XX AC ABP61231;
XX DT 20-SEP-2002 (first entry)
XX DE Anti-VEGF antibody VH1 peptide Y0243-1.
XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intraocular neovascular disorder.
XX OS Synthetic.
XX OS US2002032315-A1.
XX PN 14-MAR-2002.
XX PD 06-APR-1998; 98US-00056160.
XX PF 06-AUG-1997; 97US-0054856P.
XX PR (BACA/) BACA M.
XX PA (WELLS/) WELLS J A.
XX PA (PREST/) PRESTA L G.
XX PA (LOWM/) LOWMAN H B.
XX PA (CHEN/) CHEN Y M.
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI; 2002-517920/55.
XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX mammal, particularly for treating tumor or retinal disorders.
XX PS Example 3; Page 29; 47pp; English.
XX CC The present invention relates to humanised anti-VEGF (vascular
XX CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX CC particularly those having a tumour or a retinal disorder e.g. intraocular
XX CC neovascular disorders. The present sequence is a peptide fragment of an
XX CC anti-VEGF variant from a second generation Fab-phase library
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 62; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 4
ABP61267
ID ABP61267 standard; peptide; 10 AA.
XX AC ABP61267;
XX DT 20-SEP-2002 (first entry)
XX DE Humanised anti-VEGF antibody heavy chain variable domain, CDRH1.
XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intraocular neovascular disorder; heavy chain;
XX KW variable domain; CDRH1.

```

XX OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 XX PN US2002032315-A1.
 XX PD 14-MAR-2002.
 XX PF 06-APR-1998; 98US-00056160.
 XX PR 06-AUG-1997; 97US-0054856P.
 XX PA (BACA/) BACA M.
 PA (WELL/) WELLS J A.
 PA (PRES/) PRESTA L G.
 PA (LOWM/) LOWMAN H B.
 PA (CHEN/) CHEN Y M.
 XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX DR WPI; 2002-517920/55.
 XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX PS Claim 23; Page 31; 47pp; English.
 XX CC The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intraocular
 CC neovascular disorders. The present sequence is an exemplary heavy chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 62; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYDFTHYGMN 10
 Db 1 GYDFTHYGMN 10
 RESULT 5
 ADQ90714
 ID ADQ90714 standard; peptide; 10 AA.
 XX AC ADQ90714;
 XX DT 21-OCT-2004 (first entry)
 XX DE Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:18.
 XX KW antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytotstatic;
 KW antiinflammatory; angiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; immunomodulatory; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain; HVR1.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO2004065417-A2.
 XX PD 05-AUG-2004.
 XX PF 23-JAN-2004; 2004WO-US001844.
 XX PR 23-JAN-2003; 2003US-0442484P.
 XX PA (GETH) GENENTECH INC.
 XX PI Simmons L;
 XX DR WPI; 2004-562149/54.
 XX PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX PS Claim 13; SEQ ID NO 18; 161pp; English.
 XX CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the difference of a human subgroup
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular
 CC endothelial cell growth factor) antibody, which is used in the
 CC exemplification of the present invention.
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 62; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYDFTHYGMN 10
 Db 1 GYDFTHYGMN 10
 RESULT 6
 ADF09953
 ID ADF09953 standard; protein; 117 AA.
 XX AC ADF09953;
 XX DT 12-FEB-2004 (first entry)
 XX DE Antibody heavy chain variable region 1C28(7-4-1).
 XX KW Antibody; stability; solubility; antigen binding affinity;
 KW variable region; human.
 XX OS Homo sapiens.
 XX PN WO2003074679-A2.
 XX PD 12-SEP-2003.
 XX PF 03-MAR-2003; 2003WO-US006598.

```

XX 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX (XENC-) XENCOR.
XX PA
XX LAZAR GA, Desjarlais JR, Marshall SA, Dahiyat B;
PI WPI; 2003-722066/68.
XX DR
XX Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX Disclosure; Fig 2a; 135pp; English.
XX CC
XX The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 62; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYDFTHYGMN 10
DB 26 GYDFTHYGMN 35
RESULT 8
AAW70686
ID AAW70686 standard; peptide; 118 AA.
XX AC
XX AAW70686;
DT 27-JAN-1999 (first entry)
XX DE
XX Anti-VEGF humanised antibody variable heavy domain of variant Y0313-1.
XX Heavy variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX Synthetic.
XX Mus sp.
XX Homo sapiens.
XX WO9845331-A2.
XX 15-OCT-1998.
XX 03-APR-1998; 98WO-US006604.
XX 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX (GETH ) GENENTECH INC.
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI; 1998-568337/48.
XX DR
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX Example 3; Fig 10B; 100pp; English.
XX The present sequence represents a variable heavy domain of an affinity-

```


CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 62; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
 DB 26 GYDFTHYGMN 35
 |||||

RESULT 9
 AAW70688
 ID AAW70688 standard; peptide; 118 AA.
 XX
 AC AAW70688;
 XX
 DT 27-JAN-1999 (first entry)
 XX
 DE Anti-VEGF humanised antibody variable heavy domain of variant Y0317.
 XX
 KW Heavy variable domain; murine; humanised antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9845331-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 03-APR-1998; 98WO-US006604.
 XX
 PR 07-APR-1997; 97US-00833504.
 PR 06-AUG-1997; 97US-00908469.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX
 DR WPI; 1998-568337/48.
 XX
 PT New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states, also related nucleic acid, vectors and transformed cells.
 XX
 PS Claim 25; Fig 10B; 100pp; English.
 XX
 CC The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 62; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
 DB 26 GYDFTHYGMN 35
 |||||

RESULT 10
 AAW70682
 ID AAW70682 standard; peptide; 118 AA.
 XX
 AC AAW70682;
 XX
 DT 27-JAN-1999 (first entry)
 XX
 DE Anti-VEGF humanised antibody variable heavy domain of variant Y0243-1.
 XX
 KW Heavy variable domain; murine; humanised antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9845331-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 03-APR-1998; 98WO-US006604.
 XX
 PR 07-APR-1997; 97US-00833504.
 PR 06-AUG-1997; 97US-00908469.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX
 DR WPI; 1998-568337/48.
 XX
 PT New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states, also related nucleic acid, vectors and transformed cells.
 XX
 PS Example 3; Fig 10B; 100pp; English.
 XX
 CC The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 62; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
 DB 26 GYDFTHYGMN 35
 |||||

RESULT 11
 AAB05900

ID AC AAB05900 standard; peptide; 118 AA.
 XX AAB05900;
 XX 17-OCT-2000 (first entry)
 XX F(ab)-12 antibody variant Y0238-3 heavy chain variable domain.
 XX Humanised; F(ab)-12; heavy chain variable domain; antibody variant;
 KW phage display; randomised library; cytotatic; antiarthritis;
 KW antipsoriatic; antidiabetic; antiinflammatory; antiarteriosclerotic;
 KW vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
 KW retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
 KW diabetic retinopathy; complementarity determining region; CDR.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200029584-A1.
 XX 25-MAY-2000.
 XX 16-NOV-1999; 99WO-US027153.
 XX 18-NOV-1998; 98US-0108945P.
 XX (GETH) GENENTECH INC.
 XX Chen YM, Lowman HB, Muller Y;
 XX WPI; 2000-387797/33.
 XX Antibody variants with higher binding affinity than native antibodies
 PT useful for diagnosis, prevention and treatment of neoplastic and non-
 PT neoplastic diseases comprises amino acid insertion in hypervariable
 PT region.
 XX Disclosure; Fig 1B; 110pp; English.
 XX The present sequence is the heavy chain variable domain of the F(ab)-12
 CC antibody variant Y0238-3. F(ab)-12 is a humanised anti-vascular
 CC endothelial growth factor (VEGF) antibody. F(ab)-12 was the parent
 CC antibody used in the production of a large number of antibody variants
 CC containing randomised peptide inserts within the complementarity
 CC determining regions (CDRs). Phage display libraries were subjected to
 CC eight rounds of selection to isolate variants with an antigen binding
 CC affinity at least two-fold stronger than the binding affinity of parent
 CC antibody for the target VEGF antibody. The anti-VEGF antibody variants
 CC may be useful in diagnostic assays for detecting expression of VEGF in
 CC cells, tissue or serum. They may also be used in the prevention and
 CC treatment of neoplastic diseases such as breast cancer, lung cancer and
 CC retinoblastoma, and non-neoplastic diseases including rheumatoid
 CC arthritis, psoriasis, atherosclerosis, and diabetic and other
 CC proliferative retinopathies
 XX Sequence 118 AA;
 SQ Query Match 100.0%; Score 62; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYDFTHYGMN 10
 |||||
 Db 26 GYDFTHYGMN 35
 RESULT 12
 AAB13382
 ID AAB13382 standard; protein; 118 AA.
 XX AAB13382;
 XX 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0243-1 heavy chain variable domain.
 DE Y0243-1; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cytotatic; antirheumatic;
 KW antiarthritis; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 OS Unidentified.
 XX Key Location/Qualifiers
 FH Region 26..35
 FT /label= CDR-H1
 FT Region 50..66
 FT /label= CDR-H2
 FT Region 70..79
 FT /label= CDR-7
 FT Region 99..112
 FT /label= CDR-H3
 XX WO200037502-A2.
 PN 29-JUN-2000.
 PD 09-DEC-1999; 99WO-US029475.
 PF 22-DEC-1998; 98US-00218481.
 XX (GETH) GENENTECH INC.
 PA Van Bruggen N, Ferrara N;
 PI WPI; 2000-442646/38.
 XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.
 XX Disclosure; Fig 14B; 60pp; English.
 XX The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0243-1. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay
 XX Sequence 118 AA;
 SQ Query Match 100.0%; Score 62; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYDFTHYGMN 10
 |||||
 Db 26 GYDFTHYGMN 35
 RESULT 13
 AAB13385

ID AAB13385 standard; protein; 118 AA.
 XX AAB13385;
 AC
 DT 21-NOV-2000 (first entry)
 XX
 DE Anti-VEGF antibody Y0317 heavy chain variable domain.
 XX
 KW Y0317; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cyostatic; antirheumatic;
 KW antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Region 26..35
 FT /label= CDR-H1
 FT Region 50..66
 FT /label= CDR-H2
 FT Region 70..79
 FT /label= CDR-7
 FT Region 99..112
 FT /label= CDR-H3
 XX
 PN WO200037502-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 09-DEC-1999; 99WO-US029475.
 XX
 PR 22-DEC-1998; 98US-00218481.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Van Bruggen N, Ferrara N;
 XX
 DR WPI; 2000-442646/38.
 XX
 XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 FT diabetes and chronic inflammation in a mammal, comprises administering a
 FT human vascular endothelial cell growth factor antagonist.
 XX
 PS Disclosure; Fig 14B; 60pp; English.
 XX
 CC The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0317. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meig's syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 62; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYDFTHYGMN 10
 |||||

Db 26 GYDFTHYGMN 35
 RESULT 14
 AAB13384
 ID AAB13384 standard; protein; 118 AA.
 XX
 AC AAB13384;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Anti-VEGF antibody Y0313-1 heavy chain variable domain.
 XX
 KW Y0313-1; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cyostatic; antirheumatic;
 KW antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Region 26..35
 FT /label= CDR-H1
 FT Region 50..66
 FT /label= CDR-H2
 FT Region 70..79
 FT /label= CDR-7
 FT Region 99..112
 FT /label= CDR-H3
 XX
 PN WO200037502-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 09-DEC-1999; 99WO-US029475.
 XX
 PR 22-DEC-1998; 98US-00218481.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Van Bruggen N, Ferrara N;
 XX
 DR WPI; 2000-442646/38.
 XX
 XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 FT diabetes and chronic inflammation in a mammal, comprises administering a
 FT human vascular endothelial cell growth factor antagonist.
 XX
 PS Disclosure; Fig 14B; 60pp; English.
 XX
 CC The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0313-1. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meig's syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay
 XX
 SQ Sequence 118 AA;
 Query Match 100.0%; Score 62; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYDFTHYGMN 10
 |||||

Best Local Similarity 100.0%; Pred. No. 0.011; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
|||||
Db 26 GYDFTHYGMN 35

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYDFTHYGMN 10
|||||
Db 26 GYDFTHYGMN 35

Search completed: April 25, 2006, 06:15:09
Job time : 54.3962 secs

RESULT 15
ABP61255
ID ABP61255 standard; protein; 118 AA.
XX
AC ABP61255;
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF Y0313-1 antibody variable heavy domain.
XX
KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KW retinal disorder; intraocular neovascular disorder; Y0313-1; heavy chain;
KW variable domain.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 26..35
FT /label= CDR-H1
FT Domain 50..66
FT /label= CDR-H2
FT Domain 70..79
FT /label= CDR-7
FT Domain 99..112
FT /label= CDR-H3
XX
PN US2002032315-A1.
XX
XX 14-MAR-2002.
XX
XX 06-APR-1998; 98US-00056160.
XX
XX 06-AUG-1997; 97US-0054856P.
XX
XX (BACA/) BACA M.
XX (WELL/) WELLS J A.
XX (PRES/) PRESTA L G.
XX (LOWM/) LOWMAN H B.
XX (CHEN/) CHEN Y M.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI; 2002-517920/55.
XX
XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX mammal, particularly for treating tumor or retinal disorders.
XX
XX Example 3; Fig 10; 47pp; English.
XX
XX The present invention relates to humanised anti-VEGF (vascular
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX particularly those having a tumour or a retinal disorder e.g. intraocular
XX neovascular disorders. The present sequence is an exemplary heavy chain
XX variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 62; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.011;

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:15:41 ; Search time 8.49057 Seconds
(without alignments)
113.322 Million cell updates/sec

Title: US-10-764-428-18

Perfect score: 62

Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	77.4	93	2 C24672	Ig heavy chain V r
2	48	77.4	99	2 S26326	Ig heavy chain V r
3	48	77.4	101	2 D24672	Ig heavy chain V r
4	48	77.4	105	2 S24764	Ig heavy chain V r
5	48	77.4	105	2 S24765	Ig heavy chain V r
6	48	77.4	109	2 S26325	Ig heavy chain V r
7	48	77.4	115	2 S19968	Ig heavy chain V r
8	48	77.4	115	2 S19965	Ig heavy chain V r
9	48	77.4	119	2 A53285	Ig heavy chain V a
10	48	77.4	120	2 B42848	L6 mAb heavy chain
11	48	77.4	124	2 PH1404	Ig heavy chain V r
12	48	77.4	146	4 S33905	Ig heavy chain pre
13	48	77.4	79	2 A49021	Ig heavy chain V-X
14	46	74.2	79	2 S46460	Ig heavy chain V r
15	46	74.2	113	2 B36259	Ig heavy chain V r
16	46	74.2	117	2 S22552	Ig heavy chain V r
17	46	74.2	119	2 PH1521	Ig heavy chain V r
18	46	74.2	119	2 PH1519	Ig heavy chain V r
19	46	74.2	136	2 S35759	BHD9D10 protein -
20	46	74.2	140	2 PH1489	Ig heavy chain V r
21	45	72.6	119	2 PH1516	Ig heavy chain V r
22	45	72.6	140	2 PH1488	Ig heavy chain V r
23	45	72.6	140	2 A36194	Ig heavy chain V r
24	44	71.0	140	2 B28572	Ig heavy chain V r
25	42	67.7	76	2 B28572	Ig heavy chain V r
26	42	67.7	98	2 B24754	Ig heavy chain V r
27	42	67.7	98	2 A28572	Ig heavy chain V r
28	42	67.7	102	2 PH1491	Ig heavy chain V r
29	42	67.7	102	2 PH1490	Ig heavy chain V r

ALIGNMENTS

RESULT 1

C24672

Ig heavy chain V region (VMU-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C:Accession: C24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: C24672

A:Molecule type: DNA

A:Residues: 1-93 <WIN>

A:Cross-references: UNIPARC:UPI0000113757; GB:X03300; NID:G52375; PIDN:CNA27039.1; PID:G

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 48; DB 2; Length 93;

Best Local Similarity 80.0%; Pred. No. 0.18;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10

||| ||| |||

Db 7 GYTFTNYGMN 16

RESULT 2

S26326

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998

C:Accession: S26326

R:Stark, S.B.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26326

A:Molecule type: mRNA

A:Residues: 1-99 <STA>

A:Cross-references: UNIPARC:UPI00001769AC; EMBL:X59174

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 48; DB 2; Length 99;

Best Local Similarity 80.0%; Pred. No. 0.19;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10

||| ||| |||

Db 6 GYTFTNYGMN 15

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RESULT 3
D24672
Ig heavy chain V region (VGM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: D24672
R;Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Accession: D24672
A;Molecule type: DNA
A;Residues: 1-101 <WN>
A;Cross-references: UNIPARC:UPI0000113758; GB:X03301; NID:G51757; PIDN:CAA27040.1; PID:G
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 48; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 7 GYTFTNYGMN 16

RESULT 4
S24764
Ig heavy chain V region (subgroup XI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: S24764; S24772; S24777
R;Klages, S.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24763
A;Accession: S24764
A;Molecule type: DNA
A;Residues: 1-105 <KLA>
A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z14999
A;Accession: S24772
A;Molecule type: DNA
A;Residues: 1-105 <KLM>
A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z15011
R;Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24776
A;Accession: S24777
A;Molecule type: DNA
A;Residues: 1-105 <THO>
A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:
C;Genetics:
A;Introns: 9/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 48; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 38 GYTFTNYGMN 47

RESULT 5
S24765
Ig heavy chain V region (subgroup XI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: S24765; S24773; S24778
R;Klages, S.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24763
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A;Accession: S24765
A;Molecule type: DNA
A;Residues: 1-105 <KLA>
A;Cross-references: UNIPARC:UPI000011648E; EMBL:Z15001
A;Accession: S24773
A;Molecule type: DNA
A;Residues: 1-105 <KLW>
A;Cross-references: UNIPARC:UPI000011648B; EMBL:Z15013
R;Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A;Reference number: S24776
A;Accession: S24778
A;Molecule type: DNA
A;Residues: 1-105 <THO>
A;Cross-references: UNIPARC:UPI000011648B; EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:
C;Genetics:
A;Introns: 9/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 77.4%; Score 48; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 38 GYTFTNYGMN 47

RESULT 6
S26325
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
C;Accession: S26325
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein ei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <STA>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696F; EMBL:X59210; NID:G52080; PID:
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-88/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 0.21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 16 GYTFTNYGMN 25

RESULT 7
S19968
Ig heavy chain V region (M-T408) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19968
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <WEI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696A; EMBL:X65089
C;Superfamily: immunoglobulin homology
```

C;Keywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 21 GYTFNYGMN 30

RESULT 8

S19965 Ig heavy chain V region (M-T321) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19965

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19965

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <WEI>

A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI0000176968; EMBL:X65088

C;Superfamily: immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 19 GYTFNYGMN 28

RESULT 9

S19967 Ig heavy chain V region (M-T406) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: S19967

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19967

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-118 <WEI>

A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI0000176969; EMBL:X65090

C;Superfamily: immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 23 GYTFNYGMN 32

RESULT 10

A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C;Accession: A53285

R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc-

and their pH-reactivity profiles

A;Reference number: A53285; MUID:92017897; PMID:1922102

A;Accession: A53285

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-119 <SAW>

A;Cross-references: UNIPARC:UPI000011D0A7; GB:D12736; NID:9220595; PIDN:BA02228.1; PID:

A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIP:63299)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFNYGMN 35

RESULT 11

B42848

L6 mAb heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B42848; S33903

R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo

J. Biol. Chem. 267, 15552-15558, 1992

A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character

A;Reference number: A42848; MUID:92348410; PMID:1639794

A;Accession: B42848

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-120 <FEL>

A;Cross-references: UNIPARC:UPI0000115333; GB:M90690; NID:9195065; PIDN:AAA38146.1; PID:

A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)

A;Accession: S33903

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <PER>

A;Cross-references: UNIPARC:UPI0000115333; EMBL:M90691

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFNYGMN 35

RESULT 12

PH1404

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000

C;Accession: PH1404; PH1406

R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; T

J. Exp. Med. 176, 1209-1214, 1992

A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in

ia virus.

A;Reference number: PH1403; MUID:93018837; PMID:1402663

A;Accession: PH1404

A;Molecule type: DNA

A;Residues: 1-124 <SHI>

A;Cross-references: UNIPARC:UPI000017694C

A:Accession: PH1406
A:Molecule type: DNA
A:Residues: 115-121 <SH2>
A:Cross-references: UNIPARC:UPI000017694C
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 48; DB 2; Length 124;
Best Local Similarity 80.0%; Pred. No. 0.24;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
||| |||:||||
Db 46 GYTFTNYGMN 55

RESULT 13

Ig heavy chain precursor V region - synthetic

C:Species: synthetic
C:Date: 13-Jan-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000

C:Accession: S33905
R;Liu, A.Y.; Robinson, R.R.; Hellstrom, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstrom
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987
A:Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.
A:Reference number: S33905; MUID:87204152; PMID:3106970
A:Accession: S33905
A:Molecule type: mRNA
A:Residues: 1-146 <LIU>
A:Cross-references: UNIPARC:UPI0000114C7D; EMBL:M16072; NID:G195270; PIDN:AAA382229.1; PI

Query Match 77.4%; Score 48; DB 4; Length 146;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
||| |||:||||
Db 45 GYTFTNYGMN 54

RESULT 14

A49021

Ig heavy chain V-XI region - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C:Accession: A49021; I51454
R;Haire, R.N.; Anemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A:Reference number: A47624; MUID:90237760; PMID:2110243
A:Accession: A49021
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-79 <HA1>
A:Cross-references: UNIPARC:UPI0000114E8E; GB:M27255; NID:G214301; PIDN:AAA49777.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.2%; Score 46; DB 2; Length 79;
Best Local Similarity 80.0%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
||| |||:||||
Db 7 GYDFGSYGMN 16

RESULT 15

S46460

Ig heavy chain V region (YAC-10) - human

C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S46460
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wint
Nature Genet. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telomeric
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <COO>
A:Cross-references: UNIPARC:UPI00001165DC; EMBL:Z27509; NID:G505445; PIDN:CAA81829.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 46; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
||| |||:||||
Db 26 GYSFTTYGMN 35

Search completed: April 25, 2006, 06:26:12
Job time : 8.49057 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 53.3962 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-18
Perfect score: 62
Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	74.2	125	Q6P10 HUMAN	Q6p10 homo sapien
2	46	74.2	241	Q921A6 MOUSE	Q921a6 mus musculus
3	46	74.2	475	Q5PQSL RAT	Q5pqsl rattus norv
4	43	69.4	176	Q50PUS ENTHI	Q50pus entamoeba h
5	43	69.4	237	Q50NY4 ENTHI	Q50ny4 entamoeba h
6	43	69.4	237	Q50V47 ENTHI	Q50v47 entamoeba h
7	43	69.4	260	Q50SP0 ENTHI	Q50sp0 entamoeba h
8	43	69.4	276	Q50T72 ENTHI	Q50t72 entamoeba h
9	43	69.4	348	Q50N11 ENTHI	Q50n11 entamoeba h
10	43	69.4	486	Q840B9 SGAMM	Q840b9 cellvibrio
11	42	67.7	120	HV03 MOUSE	P01746 mus musculus
12	42	67.7	140	Q5KX50 GEOKA	Q5kx50 geobacillus
13	42	67.7	264	Q74LM7 LACJO	Q74lm7 lactobacill
14	42	67.7	515	Q70CA8 STRIR	Q70ca8 streptococc
15	42	67.7	562	Q935T8 STRIR	Q935t8 streptococc
16	42	67.7	562	Q935T8 STRIR	Q935t8 streptococc
17	41	66.1	124	Q9N0W4 RABIT	Q9n0w4 cryptotolagus
18	41	66.1	124	Q9N0W6 RABIT	Q9n0w6 cryptotolagus
19	41	66.1	162	Q6J192 9RURY	Q6j192 uncultured
20	41	66.1	313	Q752R9 ASHGO	Q752r9 ashbya goss
21	41	66.1	449	Q5CJAI CRYPO	Q5cjai cryptospori
22	41	66.1	447	Q5CXK4 CRYPV	Q5cxk4 cryptospori
23	41	66.1	454	Q82P16 STRAW	Q82p16 streptomyce
24	41	66.1	853	Q7XL98 ORYSA	Q7xl98 oryza sativ
25	41	66.1	1417	Q4UIZ2 THEAN	Q4uiz2 theileria a
26	41	66.1	1668	Q4UFD6 THEAN	Q4ufd6 theileria a
27	41	66.1	1931	Q4UPL3 THEAN	Q4upl3 theileria a
28	41	66.1	2123	Q4UHH0 THEAN	Q4uhh0 theileria a
29	41	66.1	2364	Q4UBH6 THEAN	Q4ueib theileria a
30	41	66.1	2732	Q4UJ64 THEAN	Q4uj64 theileria a
31	41	66.1	3096	Q4UCL8 THEAN	Q4ucl8 theileria a

32 40 64.5 120 2 Q920B8 MOUSE Q920e8 mus musculus
33 40 64.5 123 2 Q8VIJ1 MOUSE Q8vij1 mus musculus
34 40 64.5 244 2 Q9VBX9 DROME Q9vbx9 drosophila
35 40 64.5 286 2 Q9VBX8 DROME Q9vbx8 drosophila
36 40 64.5 387 2 Q56F03 CAUDU Q56f03 aeromonas p
37 40 64.5 465 2 Q8A7R9 BACTN Q8a7r9 bacteroides
38 40 64.5 470 1 SP63 STRPU Q8a7r9 strongyloce
39 40 64.5 474 2 Q8F5K5 COREP Q8f5k5 corynebacte
40 40 64.5 474 2 Q8NTD8 CORGL Q8ntd8 corynebacte
41 40 64.5 486 2 Q5HZY6 MOUSE Q5hzy6 mus musculus
42 40 64.5 500 2 Q5KRJ9 CRYNE Q5krf9 cryptococu
43 40 64.5 541 2 Q55OL6 CRYNE Q55ql6 cryptococu
44 40 64.5 637 2 Q91X11 MOUSE Q91x11 mus musculus
45 40 64.5 806 1 LONI BORBU Q59185 borrelia bu

ALIGNMENTS

RESULT 1
Q6P10 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q6P10; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHV7-81 protein.
GN Name=IGHV7-81;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh P.,
RA Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lymph;
RC NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032733; AAH32733.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6P10; 20-117.
DR HGNC; HGNC:5669; IGHV7-81.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 125 AA; 13913 MW; B76CE434F5A69788 CRC64;

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Query Match          74.2%; Score 46; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 45 GYSPTTYGMN 54

RESULT 2
Q921A6 MOUSE
ID Q921A6 MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-815(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RA "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1 241
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26086 MW; 02768872489C771 CRC64;

Query Match          74.2%; Score 46; DB 2; Length 241;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 26 GYTFTDYGMN 35

RESULT 3
Q5PQS1 RAT
ID Q5PQS1 RAT PRELIMINARY; PRT; 475 AA.
AC Q5PQS1
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087057; AAH87057.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 475 AA; 52118 MW; EC61093B69A96708 CRC64;

Query Match          74.2%; Score 46; DB 2; Length 475;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 45 GYTFTDYGMN 54

RESULT 4
Q50PUS ENTHI
ID Q50PUS ENTHI PRELIMINARY; PRT; 176 AA.
AC Q50PUS;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=357.t00005;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

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RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB0100022; EAL43300.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 176 AA; 20448 MW; 916FBE8A5F67B8C CRC64;

Query Match 69.4%; Score 43; DB 2; Length 176;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
DB 19 GYDFTGYGRN 28
|||||
|

RESULT 5
Q50NY4 ENTHI PRELIMINARY; PRT; 237 AA.
AC Q50NY4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=407.t00002;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB0100022; EAL43300.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 237 AA; 27296 MW; CCB644C6F61A51E1 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 237;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
DB 80 GYDFTGYGRN 89
|||||
|

RESULT 6
Q50V47 ENTHI PRELIMINARY; PRT; 238 AA.
AC Q50V47;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=196.t00002;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB01000602; EAL45460.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 238 AA; 27499 MW; 4354BED1DA574954 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 238;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
DB 81 GYDFTGYGRN 90
|||||
|

RESULT 7
Q50SP0 ENTHI PRELIMINARY; PRT; 260 AA.
AC Q50SP0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=253.t00018, 8.t00068;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB01001022; EAL43300.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 237 AA; 27296 MW; CCB644C6F61A51E1 CRC64;

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RESULT 6
Q50V47 ENTHI PRELIMINARY; PRT; 238 AA.
AC Q50V47;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=196.t00002;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB01000602; EAL45460.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 238 AA; 27499 MW; 4354BED1DA574954 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 238;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
DB 81 GYDFTGYGRN 90
|||||
|

RESULT 7
Q50SP0 ENTHI PRELIMINARY; PRT; 260 AA.
AC Q50SP0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=253.t00018, 8.t00068;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFB01000602; EAL45460.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Eukaryota; Entamoebidae; Entamoeba.
SQ SEQUENCE 238 AA; 27499 MW; 4354BED1DA574954 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 238;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
DB 81 GYDFTGYGRN 90
|||||
|

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RL Nature 433:865-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFB01000720; EAL44622.1; -; Genomic DNA.
 DR EMBL; AAFB01000442; EAL51409.1; -; Genomic_DNA.
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR000379; Ser_estrs.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 KW Hydrolase; Hypothetical protein.
 SQ SEQUENCE 260 AA; 29344 MW; 5D5298790487EC84 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 260;
 Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
 |||:||||
 Db 78 GYDVTGYGSR 87

RESULT 8
 Q50T72 ENTHI PRELIMINARY; PRT; 276 AA.
 ID Q50T72 ENTHI PRELIMINARY;
 AC Q50T72
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=240.t00009.
 OS Entamoeba histolytica HM-1.IMSS.
 CC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1.IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
 RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
 RA Fraser C.M., Hall N.;
 RA "The genome of the protist parasite Entamoeba histolytica.";
 RL Nature 433:865-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFB01000684; EAL44800.1; -; Genomic_DNA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estrs.
 DR PRINTS; PR00111; ABHYDROLASE.
 KW Hydrolase; Hypothetical protein.
 SQ SEQUENCE 276 AA; 31441 MW; 2B5F6277B5ED0942 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 276;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
 |||:||||
 Db 87 GYDVTGYGSR 96

RESULT 9
 Q50N11 ENTHI PRELIMINARY; PRT; 348 AA.
 ID Q50N11 ENTHI PRELIMINARY;
 AC Q50N11

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=437.t00002;
 OS Entamoeba histolytica HM-1.IMSS.
 CC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1.IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
 RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
 RA Fraser C.M., Hall N.;
 RA "The genome of the protist parasite Entamoeba histolytica.";
 RL Nature 433:865-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFB010001078; EAL43151.1; -; Genomic_DNA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR007093; LRR_Tp.
 DR InterPro; IPR000379; Ser_estrs.
 DR PRINTS; PR00111; ABHYDROLASE.
 KW Hydrolase; Hypothetical protein.
 SQ SEQUENCE 348 AA; 39832 MW; 64E2585020803E85 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 348;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
 |||:||||
 Db 19 GYDVTGYGSR 28

RESULT 10
 Q840B9 9GAMM PRELIMINARY; PRT; 486 AA.
 ID Q840B9 9GAMM PRELIMINARY;
 AC Q840B9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Endo-bl,4-mannanase 26B.
 GN Name=man26B;
 OS Cellvibrio japonicus.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Cellvibrio.
 OX NCBI_TaxID=155077;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22588103; PubMed=12523937; DOI=10.1042/BJ20021860;
 RA Hogg D., Pell G., Dupree P., Goubet P., Martin-Orue S.M., Armand S.,
 RA Gilbert H.J.;
 RA "The modular architecture of Cellvibrio japonicus mannanases in
 RT glycoside hydrolase families 5 and 26 points to differences in their
 RT role in mannan degradation.";
 RL Biochem. J. 371:1027-1043(2003).
 DR EMBL; AY187034; AA031762.1; -; Genomic DNA.
 DR GO; GO:0004553; F:hydrolase activity, Hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0016985; F:mannan endo-1,4-beta-mannosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006080; P:mannan metabolism; IEA.
 DR InterPro; IPR002883; Dockerin_CBD_5.

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DR InterPro: IPR00805; Glyco_hydro_26.
DR Pfam: PF02013; CEM_10; 1.
DR Pfam: PF02156; Glyco_hydro_26; 1.
DR PRINTS: PR00739; GLYDRLASE26.
SQ SEQUENCE 486 AA; 53233 MW; 0494751306D5DD70 CRC64;

Query Match 69.4%; Score 43; DB 2; Length 486;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGM 9
Db 198 GYDFTHYGM 206

RESULT 11
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.
RX MEDLINE=21528949; PubMed=11673524;
RA Parhami-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;
RT "Structural analysis of mutants of high-affinity and low-affinity p-
RT azophenylarsonate-specific antibodies generated by alanine scanning of
RT heavy chain complementarity-determining region 2."
RL J. Immunol. 167:5129-5135(2001).
CC -!- MISCELLANEOUS: From analysis of the sizes of several other
CC differentiated genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A94264; HVMG57.
CC PDB; 1JFQ; X-ray; H=1-120.
CC Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AP CRC64;

Query Match 67.7%; Score 42; DB 1; Length 120;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DR PIR; A94264; HVMG57.
DR PDB; 1JFQ; X-ray; H=1-120.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AP CRC64;

Query Match 67.7%; Score 42; DB 1; Length 140;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGM 10
Db 45 GYTFTSYGIN 54

RESULT 12
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; J00493; AAA38128.1; -; mRNA.
CC HSSP; P01747; 1JFQ.
CC SMR; P01746; 20-140.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 Ig heavy chain V region 93G7.
FT DOMAIN 20 139 Ig-like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 67.7%; Score 42; DB 1; Length 140;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGM 10
Db 45 GYTFTSYGIN 54

RESULT 13
Q5KXS0 GEOKA
ID Q5KXS0 GEOKA PRELIMINARY; PRT; 264 AA.
AC Q5KXS0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Spore-specific N-acetylmuramoyl-L-alanine amidase (Spore cortex-
DE lytic enzyme) (EC 3.5.1.28).
GN OrderedLocustNames=GK2231;
OS Geobacillus kaustophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1462;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=HTA426;
RX PubMed=15576355; DOI=10.1093/nar/gkh970;
RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
RA Matsui S., Uchiyama I.;
RT "Thermoadaptation trait revealed by the genome sequence of
RT thermophilic Geobacillus kaustophilus.";
RL Nucleic Acids Res. 32:6292-6303(2004).
DR EMBL; BA000043; BAD76516.1; -; Genomic_DNA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0008745; F:N-acetylmuramyl-L-alanine amidase activity; IEA.
DR GO; GO:0002070; P:peptidoglycan metabolism; IEA.
DR GO; GO:0009847; P:spore germination; IEA.
DR InterPro; IPR002477; PG_binding.
DR InterPro; IPR011105; SieB_hydro.
DR Pfam; PF07486; Hydrolase_2; 1.
DR Pfam; PF01471; PG_binding_1; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 264 AA; 29204 MW; 70ED5F2B46051811 CRC64;

Query Match 67.7%; Score 42; DB 2; Length 264;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYG 8
Db 110 GNDFTHYG 117
| | | | |

RESULT 14
Q74LM7_LACJO
ID Q74LM7_LACJO PRELIMINARY; PRT; 515 AA.
AC Q74LM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=LJ0156;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=333959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwielen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AB017200; AAS08138.1; -; Genomic DNA.
DR GO; GO:0003796; F:lysozyme activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR008270; Glyco_hydro_25.
DR InterPro; IPR002053; Glyco_hydro_25.
DR InterPro; IPR003646; SH3_bac.
DR Pfam; PF01183; Glyco_hydro_25; 1.
DR ProDom; PD004620; Glyco_hydro_25; 1.
DR SMART; SM00641; Glyco_25; 2.
DR SMART; SM00287; SH3b; 2.
DR PROSITE; PS00953; GLYCOSYL_HYDROL_F25; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 515 AA; 55968 MW; 0D08FB65591ACD04 CRC64;

Query Match 67.7%; Score 42; DB 2; Length 515;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
| | | | |

Db 102 GYHYTHFGSN 111

RESULT 15
Q70CAB_STRTR
ID Q70CAB_STRTR PRELIMINARY; PRT; 562 AA.
AC Q70CAB;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transfer protein.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CNR2385;
RA Pavlovic G., Burris V., Gintz B., Decaris B., Guedon G.;
RT "Evolution of genomic islands by deletion and tandem accretion by
RT site-specific recombination: ICESt1-related elements from
RT Streptococcus thermophilus.";
RL Microbiology 50:759-774(2004).
DR EMBL; AJ586568; CAE52361.1; -; Genomic_DNA.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
DR PROSITE; PS50901; FTSK; 1.
DR PROSITE; PS50901; FTSK; 1.
SQ SEQUENCE 562 AA; 65116 MW; A8A817063326D21B CRC64;

Query Match 67.7%; Score 42; DB 2; Length 562;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGM 9
| | | | |
Db 294 GKNFTHYGM 302

Search completed: April 25, 2006, 06:24:42
Job time : 56.3962 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 13.4906 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-18

Perfect score: 62

Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/iaa/5 COMB.pep:*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/PCRTUS COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pep:*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	10	2	US-08-908-469-86
2	62	100.0	10	2	US-08-908-469-128
3	62	100.0	118	2	US-09-440-781-97
4	62	100.0	118	2	US-08-908-469-112
5	62	100.0	118	2	US-08-908-469-116
6	62	100.0	118	2	US-08-908-469-118
7	62	100.0	121	2	US-09-440-781-99
8	58	93.5	10	2	US-08-908-469-88
9	58	93.5	10	2	US-08-908-469-90
10	55	88.7	10	2	US-08-908-469-89
11	54	87.1	10	2	US-08-908-469-91
12	52	83.9	10	2	US-08-908-469-87
13	51	82.3	10	2	US-09-440-781-19
14	49	79.0	160	2	US-09-318-786-35
15	48	77.4	10	2	US-09-440-781-20
16	48	77.4	10	2	US-08-908-469-1
17	48	77.4	92	2	US-08-783-853A-84
18	48	77.4	92	2	US-09-344-050-84
19	48	77.4	112	2	US-08-783-853A-20
20	48	77.4	112	2	US-09-344-050-20
21	48	77.4	118	1	US-08-425-336-124
22	48	77.4	118	1	US-08-425-336-126
23	48	77.4	118	1	US-08-488-113B-124
24	48	77.4	118	1	US-08-488-113B-126
25	48	77.4	118	1	US-08-477-484B-124
26	48	77.4	118	1	US-08-477-484B-126
27	48	77.4	118	1	US-08-107-669D-28

28	48	77.4	118	1	US-08-107-669D-29	Sequence 29, Appl
29	48	77.4	118	1	US-08-107-669D-66	Sequence 66, Appl
30	48	77.4	118	1	US-08-107-669D-67	Sequence 67, Appl
31	48	77.4	118	1	US-08-472-788A-28	Sequence 28, Appl
32	48	77.4	118	1	US-08-472-788A-29	Sequence 29, Appl
33	48	77.4	118	1	US-08-472-788A-88	Sequence 88, Appl
34	48	77.4	118	1	US-08-472-788A-89	Sequence 89, Appl
35	48	77.4	118	1	US-08-477-531B-28	Sequence 28, Appl
36	48	77.4	118	1	US-08-477-531B-29	Sequence 29, Appl
37	48	77.4	118	1	US-08-477-531B-66	Sequence 66, Appl
38	48	77.4	118	1	US-08-477-531B-67	Sequence 67, Appl
39	48	77.4	118	1	US-08-646-360-124	Sequence 124, App
40	48	77.4	118	1	US-08-646-360-126	Sequence 126, App
41	48	77.4	118	1	US-08-082-842A-28	Sequence 28, Appl
42	48	77.4	118	1	US-08-082-842A-29	Sequence 29, Appl
43	48	77.4	118	1	US-08-082-842A-88	Sequence 88, Appl
44	48	77.4	118	1	US-08-082-842A-89	Sequence 89, Appl
45	48	77.4	118	2	US-08-839-765-124	Sequence 124, App

ALIGNMENTS

RESULT 1
US-08-908-469-86
; Sequence 86, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS: 131
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-08-908-469-86

Query Match 100.0%; Score 62; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYDFTHYGMN 10
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Db      1 GYDFTHYGMN 10

RESULT 2
US-08-908-469-128
; Sequence 128, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-08-908-469-128
Query Match      100.0%; Score 62; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      |||||
Db      1 GYDFTHYGMN 10

RESULT 3
US-09-440-781-97
; Sequence 97, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 97
; LENGTH: 118
Query Match      100.0%; Score 62; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      |||||
Db      1 GYDFTHYGMN 10

RESULT 4
US-08-908-469-112
; Sequence 112, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-908-469-112
Query Match      100.0%; Score 62; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      |||||
Db      26 GYDFTHYGMN 35

RESULT 5
US-08-908-469-112
; Sequence 112, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-908-469-112
Query Match      100.0%; Score 62; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      |||||
Db      26 GYDFTHYGMN 35
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US-08-908-469-116
; Sequence 116, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-08-908-469-118
Query Match 100.0%; Score 62; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
RESULT 7
US-09-440-781-99
; Sequence 99, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 99
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-121
; OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-99
Query Match 100.0%; Score 62; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
RESULT 8
US-08-908-469-88
; Sequence 88, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.

US-08-908-469-116
; Sequence 116, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-08-908-469-118
Query Match 100.0%; Score 62; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
RESULT 6
US-08-908-469-118
; Sequence 118, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```
; ; Presta, Leonard G.
; ; Lowman, Henry B.
; ; Chen, Yvonne M.
; ;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-08-908-469-88
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; Query Match 93.5%; Score 58; DB 2; Length 10;
; Best Local Similarity 90.0%; Pred. No. 0.0019;
; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GYDFTHYGMN 10
; Db 1 GYDFSHYGMN 10
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; RESULT 10
;
; US-08-908-469-89
; Sequence 89, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-08-908-469-90
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; Query Match 93.5%; Score 58; DB 2; Length 10;
; Best Local Similarity 90.0%; Pred. No. 0.0019;
; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 GYDFTHYGMN 10
; Db 1 GYDFSHYGMN 10
;
; RESULT 10
;
; US-08-908-469-89
; Sequence 89, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-08-908-469-90
;
; Query Match 93.5%; Score 58; DB 2; Length 10;
; Best Local Similarity 90.0%; Pred. No. 0.0019;
; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 GYDFTHYGMN 10
; Db 1 GYDFSHYGMN 10
;
; RESULT 9
;
; US-08-908-469-90
; Sequence 90, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 89:

US-08-908-469-89
Query Match 88.7%; Score 55; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFGHYGMN 10

RESULT 11

US-08-908-469-91
; Sequence 91, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-08-908-469-91

Query Match 87.1%; Score 54; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.0084;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFSHYGMN 10

RESULT 12

US-08-908-469-87
; Sequence 87, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel

Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-08-908-469-87

Query Match 83.9%; Score 52; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFQHYGMN 10

RESULT 13
US-09-440-781-19
; Sequence 19, Application US/09440781
; Patent No. 6832926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; NAME/KEY: artificial
; LOCATION: 1-10
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-19

Query Match 82.3%; Score 51; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.026;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
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Db 1 GYDFTNYGIN 10

RESULT 14

US-09-318-786-35
; Sequence 35, Application US/09318786
; Patent No. 6472147
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D
; APPLICANT: Wirsching, Peter
; APPLICANT: Lerner, Richard A
; APPLICANT: Gao, Changshou
; TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
; TITLE OF INVENTION: FILAMENTOUS PHAGE USING pVII AND pIX, COMPOSITIONS,
; TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
; FILE REFERENCE: TSR03058
; CURRENT APPLICATION NUMBER: US/09/318,786
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion
; OTHER INFORMATION: polypeptide
US-09-318-786-35

Query Match 79.0%; Score 49; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
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Db 28 GYSFTNYGMN 37

RESULT 15

US-09-440-781-20
; Sequence 20, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P146981
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-10
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-20

Query Match 77.4%; Score 48; DB 2; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.079;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
|||||:|:|
Db 1 GYDFTNYGIN 10

Search completed: April 25, 2006, 06:28:40
Job time : 13.4906 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:58:17 ; Search time 43.5849 Seconds
(without alignments)
95.866 Million cell updates/sec

Title: US-10-764-428-18
Perfect score: 62
Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
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2: /cgm2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	10	3	US-09-056-160B-86
2	62	100.0	10	3	US-09-056-160B-128
3	62	100.0	10	4	US-10-234-671-86
4	62	100.0	10	4	US-10-234-671-126
5	62	100.0	10	5	US-10-764-428-18
6	62	100.0	10	5	US-10-974-591-86
7	62	100.0	10	5	US-10-974-591-126
8	62	100.0	117	4	US-10-379-392-58
9	62	100.0	117	4	US-10-379-392-122
10	62	100.0	117	4	US-10-379-392-124
11	62	100.0	117	4	US-10-379-392-130
12	62	100.0	118	3	US-09-056-160B-112
13	62	100.0	118	3	US-09-056-160B-116
14	62	100.0	118	3	US-09-056-160B-118
15	62	100.0	118	4	US-10-234-671-110
16	62	100.0	118	4	US-10-234-671-114
17	62	100.0	118	4	US-10-234-671-116
18	62	100.0	118	4	US-10-624-153-97
19	62	100.0	118	5	US-10-683-043-10
20	62	100.0	118	5	US-10-683-043-12
21	62	100.0	118	5	US-10-683-043-13
22	62	100.0	118	5	US-10-974-591-110
23	62	100.0	118	5	US-10-974-591-114
24	62	100.0	118	5	US-10-974-591-116
25	62	100.0	121	4	US-10-624-153-99
26	62	100.0	121	5	US-10-683-043-16
27	62	100.0	123	4	US-10-153-159-3

Sequence 3, Appli
Sequence 3, Appli
Sequence 56, Appl
Sequence 136, App
Sequence 138, App
Sequence 140, App
Sequence 148, App
Sequence 9, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 7, Appli
Sequence 13, Appl
Sequence 127, App
Sequence 95, Appl
Sequence 88, Appl
Sequence 90, Appl
Sequence 88, Appl
Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-09-056-160B-86
; Sequence 86, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS: 131
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM: 3.5 inch, 1.44 Mb floppy disk
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet B.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-86

Query Match 100.0%; Score 62; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYDFTHYGMN 10

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Db      1 GYDFTHYGMN 10

RESULT 2
US-09-056-160B-128
; Sequence 128, Application US/09056160B
; Patent No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-056-160B-128

Query Match      100.0%; Score 62; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYDFTHYGMN 10
Db      1 GYDFTHYGMN 10

RESULT 3
US-10-234-671-86
; Sequence 86, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-10-234-671-86

Query Match      100.0%; Score 62; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYDFTHYGMN 10
Db      1 GYDFTHYGMN 10

RESULT 4
US-10-234-671-126
; Sequence 126, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-234-671-126
Query Match 100.0%; Score 62; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 5
US-10-764-428-18
; Sequence 18, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; FILE REFERENCE: 11669.120USU1
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Y0317 VH HVRI residues 26-35
US-10-764-428-18
Query Match 100.0%; Score 62; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 6
US-10-974-591-86
; Sequence 86, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
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; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-974-591-86
Query Match 100.0%; Score 62; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 7
US-10-974-591-126
; Sequence 126, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-974-591-126

Query Match 100.0%; Score 62; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
Db 1 GYDFTHYGMN 10

RESULT 8
US-10-379-392-58
; Sequence 58, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-58

Query Match 100.0%; Score 62; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

US-10-379-392-124
; Sequence 124, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-124

Query Match 100.0%; Score 62; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

US-10-379-392-130
; Sequence 130, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-124

Query Match 100.0%; Score 62; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

US-10-379-392-122
; Sequence 122, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-122

Query Match 100.0%; Score 62; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
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Publication No. US20040110236A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basim I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patent in version 3.2
SEQ ID NO 130
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (45)-(45)
OTHER INFORMATION: Xaa at position 45 can be Leu or Met
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (95)-(95)
OTHER INFORMATION: Xaa at position 95 can be Phe, Tyr or Met
US-10-379-392-130
Query Match 100.0%; Score 62; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
RESULT 12
US-09-056-160B-112
Sequence 112, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-116
Query Match 100.0%; Score 62; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35
RESULT 13
US-09-056-160B-116
Sequence 116, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-116
Query Match 100.0%; Score 62; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-112
Query Match 100.0%; Score 62; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

RESULT 13
US-09-056-160B-116
Sequence 116, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-116

Query Match 100.0%; Score 62; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
Db 26 GYDFTHYGMN 35

Db 26 GYDFTHYGMN 35

RESULT 14

US-09-056-160B-118
; Sequence 118, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haseak, Janet B.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: F1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-118

Query Match 100.0%; Score 62; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10

Db 26 GYDFTHYGMN 35

RESULT 15

US-10-234-671-110
; Sequence 110, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-Apr-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-Apr-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: F1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-234-671-110

Query Match 100.0%; Score 62; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10

Db 26 GYDFTHYGMN 35

Search completed: April 25, 2006, 07:08:48
Job time : 43.5849 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 6.41509 Seconds
(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-18

Perfect score: 62

Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/prodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/prodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/prodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/prodata/1/pubpaa/FCI NEW PUB.pep.*
- 5: /SIDSS/prodata/1/pubpaa/US09 NEW PUB.pep.*
- 6: /SIDSS/prodata/1/pubpaa/US10 NEW PUB.pep.*
- 7: /SIDSS/prodata/1/pubpaa/US11 NEW PUB.pep.*
- 8: /SIDSS/prodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	118	6	US-10-648-816-10
2	62	100.0	118	6	US-10-648-816-12
3	62	100.0	118	6	US-10-648-816-13
4	62	100.0	121	6	US-10-648-816-16
5	62	100.0	123	7	US-11-208-422-12
6	51	82.3	256	7	US-11-054-515-2080
7	51	82.3	256	7	US-11-266-444-2080
8	48	77.4	92	7	US-11-240-195-84
9	48	77.4	112	7	US-11-240-195-20
10	48	77.4	116	7	US-11-174-186-2
11	48	77.4	116	7	US-11-174-186-4
12	48	77.4	116	7	US-11-174-186-6
13	48	77.4	116	7	US-11-174-186-17
14	48	77.4	116	7	US-11-174-186-18
15	48	77.4	116	7	US-11-174-186-19
16	48	77.4	116	7	US-11-174-186-20
17	48	77.4	116	7	US-11-174-186-21
18	48	77.4	116	7	US-11-174-186-22
19	48	77.4	116	7	US-11-174-186-23
20	48	77.4	116	7	US-11-174-186-24
21	48	77.4	116	7	US-11-174-186-25
22	48	77.4	116	7	US-11-174-186-26
23	48	77.4	117	7	US-11-174-186-35
24	48	77.4	117	7	US-11-037-199-32
25	48	77.4	118	6	US-10-648-816-9

ALIGNMENTS

RESULT 1

US-10-648-816-10
; Sequence 10, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-10

Query Match 100.0%; Score 62; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GYDFTHYGMN	10
Db	26	GYDFTHYGMN	35

RESULT 2

US-10-648-816-12
; Sequence 12, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22

Sequence 14, Appl
Sequence 15, Appl
Sequence 7, Appl
Sequence 31, Appl
Sequence 52, Appl
Sequence 111, App
Sequence 109, App
Sequence 8, Appl
Sequence 10, Appl
Sequence 89, Appl
Sequence 41, Appl
Sequence 58, Appl
Sequence 53, Appl
Sequence 58, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 68, Appl
Sequence 70, Appl
Sequence 848, App
Sequence 848, App

26	48	77.4	118	6	US-10-648-816-14
27	48	77.4	121	7	US-10-648-816-15
28	48	77.4	121	7	US-11-240-195-7
29	48	77.4	121	7	US-11-240-195-31
30	48	77.4	121	7	US-11-240-195-52
31	48	77.4	121	7	US-11-240-195-111
32	48	77.4	123	7	US-11-240-195-109
33	48	77.4	123	7	US-11-208-422-8
34	48	77.4	123	7	US-11-208-422-10
35	48	77.4	140	7	US-11-240-195-89
36	48	77.4	579	7	US-11-174-186-41
37	46	74.2	98	7	US-11-084-554-58
38	46	74.2	98	7	US-11-004-590-53
39	46	74.2	98	7	US-11-136-250-58
40	46	74.2	259	6	US-10-512-184-31
41	46	74.2	259	6	US-10-512-184-33
42	46	74.2	329	6	US-10-512-184-68
43	46	74.2	329	6	US-10-512-184-70
44	45	72.6	248	7	US-11-054-515-848
45	45	72.6	248	7	US-11-266-444-848

; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-12

Query Match 100.0%; Score 62; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
| | | | | | | | | |
Db 26 GYDFTHYGMN 35

RESULT 3

US-10-648-816-13
; Sequence 13, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 13
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-13

Query Match 100.0%; Score 62; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
| | | | | | | | | |
Db 26 GYDFTHYGMN 35

RESULT 4

US-10-648-816-16
; Sequence 16, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 16
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-16

Query Match 100.0%; Score 62; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00095;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYDFTHYGMN 10
| | | | | | | | | |
Db 26 GYDFTHYGMN 35

RESULT 5

US-11-208-422-12
; Sequence 12, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-12

Query Match 100.0%; Score 62; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
| | | | | | | | | |
Db 26 GYDFTHYGMN 35

RESULT 6

US-11-054-515-2080
; Sequence 2080, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247

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; SEQ ID NO 2080
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2080

Query Match      82.3%; Score 51; DB 7; Length 256;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      || |||||:|
Db      26 GYPFTHYGMN 35

RESULT 7
US-11-266-444-2080
; Sequence 2080, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2080
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2080

Query Match      82.3%; Score 51; DB 7; Length 256;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      || |||||:|
Db      26 GYPFTHYGMN 35

RESULT 8
US-11-240-195-84
; Sequence 84, Application US/11240195
; Publication No. US20060057140A1
; GENERAL INFORMATION:
; APPLICANT: Feuerstein, Giora Z.
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; FILE REFERENCE: P50816-1
; CURRENT APPLICATION NUMBER: US/11/240,195
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/10/430,176
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 09/817,960
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/359,202
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 60/095,714
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-84

Query Match      77.4%; Score 48; DB 7; Length 112;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYDFTHYGMN 10
      || |||||:|
Db      23 GYTFTNYGMN 32
```

```
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-84

Query Match      77.4%; Score 48; DB 7; Length 92;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GYDFTHYGMN 10
      || |||||:|
Db      3 GYTFTNYGMN 12

RESULT 9
US-11-240-195-20
; Sequence 20, Application US/11240195
; Publication No. US20060057140A1
; GENERAL INFORMATION:
; APPLICANT: Feuerstein, Giora Z.
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; FILE REFERENCE: P50816-1
; CURRENT APPLICATION NUMBER: US/11/240,195
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/10/430,176
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 09/817,960
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/359,202
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 60/095,714
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-20
```

```
QY      1 GYDFTHYGMN 10
      || |||||:|
Db      23 GYTFTNYGMN 32
```

```
RESULT 10
US-11-174-186-2
; Sequence 2, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH mouse
US-11-174-186-2
Query Match 77.48; Score 48; DB 7; Length 116;
Best Local Similarity 80.08; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYDFTHYGMN 10
||| ||| |||
Db 26 GYTFNTYGMN 35

RESULT 11
US-11-174-186-4
; Sequence 4, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable heavy chain sequence in the EpcAM antibody
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85)..(85)
```

```
; LOCATION: (17)..(17)
; OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (38)..(38)
; OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (43)..(43)
; OTHER INFORMATION: wherein Xaa at position 43 is a lysine or a glutamine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (63)..(63)
; OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (68)..(68)
; OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: wherein Xaa at position 71 is a serine or a threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (72)..(72)
; OTHER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (76)..(76)
; OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (79)..(79)
; OTHER INFORMATION: wherein Xaa at position 79 is an alanine or a leucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (80)..(80)
; OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (83)..(83)
; OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84)..(84)
; OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85)..(85)
```

```
; OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)..(88)
; OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or a
; OTHER INFORMATION: serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100)..(100)
; OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108)..(108)
; OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (111)..(111)
; OTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine
; US-11-174-186-4
```

```
Query Match 77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFPTYGMN 35
```

RESULT 12

```
US-11-174-186-6
; Sequence 6, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingl
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: heavy sequence consensus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (17)..(17)
; OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (38)..(38)
; OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (63)..(63)
; OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)..(68)
; OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (76)..(76)
; OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)..(80)
; OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (83)..(83)
; OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (84)..(84)
; OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (85)..(85)
; OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)..(88)
; OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or a
; OTHER INFORMATION: serine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
; FEATURE:
; NAME/KEY: misc_feature
```

; LOCATION: (108)..(108)
; OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
US-11-174-186-6

Query Match 77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFTNYGMN 35

RESULT 13

US-11-174-186-17
; Sequence 17, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH6 heavy chain
US-11-174-186-17

Query Match 77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFTNYGMN 35

RESULT 14

US-11-174-186-18
; Sequence 18, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH7 heavy chain
US-11-174-186-18

Query Match 77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFTNYGMN 35

RESULT 15

US-11-174-186-19
; Sequence 19, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH2.5 heavy chain
US-11-174-186-19

Query Match 77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYDFTHYGMN 10
|||:||||
Db 26 GYTFTNYGMN 35

Search completed: April 25, 2006, 07:10:02
Job time : 7.58176 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 58.7358 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-19
Perfect score: 64
Sequence: 1 GYSITGYSWN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	11	ADQ90715	Adq90715 Anti-VSGF
2	64	100.0	114	AAW95656	AAW95656 Mus muscu
3	64	100.0	114	AAW95657	AAW95657 Mus muscu
4	64	100.0	114	AAW76946	AAW76946 Variable
5	64	100.0	114	AAW76945	AAW76945 Variable
6	64	100.0	114	ADN07033	ADN07033 Anti-IGF
7	64	100.0	114	ADN07032	ADN07032 Anti-IGF
8	64	100.0	114	ADW00854	ADW00854 Human ant
9	64	100.0	114	ADW00855	ADW00855 Human ant
10	64	100.0	114	ADW79890	ADW79890 Anti-IGF
11	64	100.0	114	ADW79889	ADW79889 Anti-IGF
12	64	100.0	119	AAC20095	AAC20095 Protein e
13	64	100.0	121	AAW95647	AAW95647 Mus muscu
14	64	100.0	121	AAW95648	AAW95648 Mus muscu
15	64	100.0	121	AAW76936	AAW76936 Variable
16	64	100.0	121	AAW76937	AAW76937 Variable
17	64	100.0	121	ADN07024	ADN07024 Murine an
18	64	100.0	121	ADN07023	ADN07023 Murine an
19	64	100.0	121	ADW00645	ADW00645 Murine Ma
20	64	100.0	121	ADW00646	ADW00646 Human F(a
21	64	100.0	134	AAW33306	AAW33306 MaB11 hea
22	64	100.0	134	AAW85194	AAW85194 Heavy cha
23	64	100.0	229	AAW95666	AAW95666 Mus muscu
24	64	100.0	229	AAW95665	AAW95665 Mus muscu

25	64	100.0	229	4	AAW76954	AAW76954 Variable
26	64	100.0	229	4	AAW76955	AAW76955 Variable
27	64	100.0	229	8	ADN07041	ADN07041 Anti-IGF
28	64	100.0	229	8	ADN07067	ADN07067 F(ab)-pha
29	64	100.0	229	8	ADN07042	ADN07042 Anti-IGF
30	64	100.0	229	9	ADW00664	ADW00664 Human ant
31	64	100.0	229	9	ADW00663	ADW00663 Human ant
32	64	100.0	229	9	ADW00689	ADW00689 Expressio
33	64	100.0	229	9	ADW00694	ADW00694 Human ant
34	64	100.0	229	9	ADW00693	ADW00693 Human ant
35	64	100.0	229	9	ADW79899	ADW79899 Anti-IGF
36	64	100.0	229	9	ADW79898	ADW79898 Anti-IGF
37	64	100.0	233	2	AAW95671	AAW95671 Mus muscu
38	64	100.0	233	2	AAW95670	AAW95670 Mus muscu
39	64	100.0	233	4	AAW76959	AAW76959 Variable
40	64	100.0	233	4	AAW76960	AAW76960 Variable
41	64	100.0	233	8	ADN07046	ADN07046 Anti-IGF
42	64	100.0	233	8	ADN07047	ADN07047 Anti-IGF
43	64	100.0	233	9	ADW00668	ADW00668 Human ant
44	64	100.0	233	9	ADW00669	ADW00669 Human ant
45	64	100.0	233	9	ADW79903	ADW79903 Anti-IGF

ALIGNMENTS

RESULT 1
ADQ90715
ID ADQ90715 standard; peptide; 11 AA.
XX AC ADQ90715;
XX AC
DT 21-OCT-2004 (first entry)
DE Anti-VEGF antibody heavy chain HVRI peptide SEQ ID NO:19.
XX
KW antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytotstatic;
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; heavy chain; HVRI.
XX Homo sapiens.
OS Synthetic.
XX WO2004065417-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001844.
XX
PR 23-JAN-2003; 2003US-0442484P.
XX
PA (GETH) GENENTECH INC.
XX
PI Simmons L;
XX
XX WPI; 2004-562149/54.
DR
XX
PT Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.
XX
PS Claim 13; SEQ ID NO 19; 161pp; English.
XX
CC The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (PR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified PR in the method described above has a substitution of at least one amino acid

CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular
 CC endothelial cell growth factor) antibody, which is used in the
 CC exemplification of the present invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 64; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00063;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 1 GYSITSGYSWN 11

RESULT 2
 AAW95656
 ID AAW95656 standard; protein; 114 AA.

XX AC AAW95656;

XX DT 08-JUN-1999 (first entry)

XX DE Mus musculus anti-IgE e27 variable heavy chain.

XX KW Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria.

XX OS Mus musculus.

XX PN WO9901556-A2.

XX PD 14-JAN-1999.

XX PF 30-JUN-1998; 98WO-US013410.

XX PR 02-JUL-1997; 97US-00887352.

XX PA (GETH) GENENTECH INC.

XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.

XX PS Disclosure; Page 90-91; 129pp; English.

XX The sequence is that of the variable heavy chain of e27. It was used as
 CC part of a method to improve the affinity of anti-IgE antibodies such as
 CC e26 and e27. The e26 and e27 antibodies can be used for reducing or
 CC preventing IgE mediated production of histamine in a mammal. They can be

CC used for treating a disorder mediated by IgE such as hypersensitivity,
 CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
 CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
 CC for affinity purification, detection and diagnosis

XX SQ Sequence 114 AA;

Query Match 100.0%; Score 64; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 26 GYSITSGYSWN 36

RESULT 3
 AAW95657
 ID AAW95657 standard; protein; 114 AA.

XX AC AAW95657;

XX DT 08-JUN-1999 (first entry)

XX DE Mus musculus anti-IgE e25, e26 & e426 variable heavy chain.

XX KW Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria.

XX OS Mus musculus.

XX PN WO9901556-A2.

XX PD 14-JAN-1999.

XX PF 30-JUN-1998; 98WO-US013410.

XX PR 02-JUL-1997; 97US-00887352.

XX PA (GETH) GENENTECH INC.

XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.

XX PS Disclosure; Page 91; 129pp; English.

XX The sequence is that of the variable heavy chain of e25, e26 and e426. It
 CC was used as part of a method to improve the affinity of anti-IgE
 CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
 CC for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis

XX SQ Sequence 114 AA;

Query Match 100.0%; Score 64; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 26 GYSITSGYSWN 36

RESULT 4
 AAB76946
 ID AAB76946 standard; protein; 114 AA.
 XX
 AC AAB76946;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Variable heavy chain sequence of e25, e26 and e426 SEQ ID 12.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 XX antinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 XX conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-00109207.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
 XX properties, produced by substituting aspartyl residues in unimproved
 XX immunoglobulin E prone to isomerization by other residues by affinity
 XX maturation with phage display.
 XX
 PS Disclosure; Fig 2; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules; and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 SQ Sequence 114 AA;
 Query Match 100.0%; Score 64; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYSITSGYSWN 11
 DB 26 GYSITSGYSWN 36
 RESULT 5
 AAB76945
 ID AAB76945 standard; protein; 114 AA.
 XX

AC AAB76945;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Variable heavy chain sequence of e27 SEQ ID 11.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 XX antinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 XX conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-00109207.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
 XX properties, produced by substituting aspartyl residues in unimproved
 XX immunoglobulin E prone to isomerization by other residues by affinity
 XX maturation with phage display.
 XX
 PS Disclosure; Fig 2; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules; and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 SQ Sequence 114 AA;
 Query Match 100.0%; Score 64; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYSITSGYSWN 11
 DB 26 GYSITSGYSWN 36
 RESULT 6
 ADN07033
 ID ADN07033 standard; protein; 114 AA.
 XX
 AC ADN07033;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Anti-IgE antibody e25, e26 and e426 variable heavy chain domain (VH).
 XX

KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable heavy chain domain; VH.
 XX Unidentified.
 XX OS
 XX
 XX Key Location/Qualifiers
 XX Region 26..36
 XX /label= CDR-H1
 XX Region 51..66
 XX /label= CDR-H2
 XX Region 99..110
 XX /label= CDR-H3
 XX US6723833-B1.
 XX PN
 XX XX
 XX 20-APR-2004.
 XX PD
 XX XX
 XX 17-NOV-2000; 2000US-00716028.
 XX PF
 XX XX
 XX 02-JUL-1997; 97US-0051554P.
 XX PR
 XX 30-JUN-1998; 98US-00109207.
 XX XX
 XX (GETH) GENENTECH INC.
 XX PA
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX PI
 XX WPI; 2004-326922/30.
 XX DR
 XX XX
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.
 XX PT
 XX Disclosure; SEQ ID NO 12; 89pp; English.
 XX PS
 XX The invention relates to therapeutic compositions comprising anti-IgE
 XX antibody or IgE binding fragment in combination with an adjunct
 XX immunosuppressive agent. The composition is useful for treating IgE-
 XX mediated disorders. The disorders include atopic allergy associated with
 XX anaphylactic hypersensitivity and asthma, allergic rhinitis and
 XX conjunctivitis, eczema, urticaria and food allergies. The present
 XX sequence is an anti-IgE antibody variable heavy chain domain (VH).
 XX CC
 XX Sequence 114 AA;
 XX
 XX Query Match 100.0%; Score 64; DB 8; Length 114;
 XX Best Local Similarity 100.0%; Pred. No. 0.0083;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYSITSGYSWN 11
 Db |||||
 26 GYSITSGYSWN 36
 RESULT 7
 ADN07032
 ID ADN07032 standard; protein; 114 AA.
 XX AC
 XX ADN07032;
 XX DT
 XX 01-JUL-2004 (first entry)
 XX DE
 XX Anti-IgE antibody e27 variable heavy chain domain (VH).
 XX
 XX Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable heavy chain domain; VH.
 XX Unidentified.
 XX OS
 XX Key Location/Qualifiers

FT Region 26..36
 FT /label= CDR-H1
 FT Region 51..66
 FT /label= CDR-H2
 FT Region 99..110
 FT /label= CDR-H3
 XX US6723833-B1.
 XX PN
 XX XX
 XX 20-APR-2004.
 XX PD
 XX XX
 XX 17-NOV-2000; 2000US-00716028.
 XX PF
 XX XX
 XX 02-JUL-1997; 97US-0051554P.
 XX PR
 XX 30-JUN-1998; 98US-00109207.
 XX XX
 XX (GETH) GENENTECH INC.
 XX PA
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX PI
 XX WPI; 2004-326922/30.
 XX DR
 XX XX
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.
 XX PT
 XX Disclosure; SEQ ID NO 11; 89pp; English.
 XX PS
 XX The invention relates to therapeutic compositions comprising anti-IgE
 XX antibody or IgE binding fragment in combination with an adjunct
 XX immunosuppressive agent. The composition is useful for treating IgE-
 XX mediated disorders. The disorders include atopic allergy associated with
 XX anaphylactic hypersensitivity and asthma, allergic rhinitis and
 XX conjunctivitis, eczema, urticaria and food allergies. The present
 XX sequence is an anti-IgE antibody variable heavy chain domain (VH).
 XX CC
 XX Sequence 114 AA;
 XX
 XX Query Match 100.0%; Score 64; DB 8; Length 114;
 XX Best Local Similarity 100.0%; Pred. No. 0.0083;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYSITSGYSWN 11
 Db |||||
 26 GYSITSGYSWN 36
 RESULT 8
 ADW00654
 ID ADW00654 standard; protein; 114 AA.
 XX AC
 XX ADW00654;
 XX DT
 XX 10-MAR-2005 (first entry)
 XX DE
 XX Human anti-IgE antibody e27 heavy chain variable region protein.
 XX
 XX Chemotherapy; IgE-mediated disorder; asthma; allergic rhinitis; eczema;
 KW urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity;
 KW antiasthmatic; antiallergic; dermatological; antibacterial;
 KW immune disorder; inflammation; ear disease; nose disease; throat disease;
 KW respiratory disease; antiinflammatory; dermatological disease;
 KW immunosuppressive; antibody.
 XX OS
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Region 24..36
 XX /note= "CDR (Complementarity-determining region)-H1"
 XX FT
 XX Region 51..66
 XX /note= "CDR (Complementarity-determining region)-H2"
 XX FT
 XX Region 99..110
 XX /note= "CDR (Complementarity-determining region)-H3"
 XX FT

```

XX FN US2004259077-A1.
XX PD 23-DEC-2004.
XX PF 02-MAR-2004; 2004US-00791619.
XX XX 02-JUL-1997; 97US-0051554P.
XX PR 30-JUN-1998; 98US-00109207.
XX PD 17-NOV-2000; 2000US-00716028.
XX PF (GETH ) GENENTECH INC.
XX XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX PI WPI; 2005-038757/04.
XX DR
XX XX Treating an IgG-mediated disorder, e.g. asthma, allergic rhinitis,
XX PT eczema, urticaria, food allergies, or hypersensitivity, by administering
XX PT an anti-IgE antibody or its antigen-binding fragment.
XX XX
XX PS Disclosure; SEQ ID NO 11; 92pp; English.
XX XX The present invention relates to a method for treating an IgE-mediated
XX CC disorder. The method involves administering a therapeutical amount of an
XX CC anti-IgE antibody or its IgE binding fragment. The invention is useful
XX CC for treating an IgE-mediated disorder e.g. asthma, allergic rhinitis,
XX CC eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic
XX CC hypersensitivity. The present sequence is the human anti-IgE antibody e27
XX CC heavy chain variable region protein.
XX SQ Sequence 114 AA;
XX Query Match 100.0%; Score 64; DB 9; Length 114;
XX Best Local Similarity 100.0%; Pred. No. 0.0083;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSITSGYSWN 11
DB |||||
26 GYSITSGYSWN 36

RESULT 9
ADW00655
ID ADW00655 standard; protein; 114 AA.
XX AC ADW00655;
XX DT 10-MAR-2005 (first entry)
XX DE Human anti-IgE antibody e26, e27 and e426 variable heavy chain protein.
XX XX
XX KW Chemotherapy; IgG-mediated disorder; asthma; allergic rhinitis; eczema;
XX KW urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity;
XX KW antiasthmatic; antiallergic; dermatological; antibacterial;
XX KW immune disorder; inflammation; ear disease; nose disease; throat disease;
XX KW respiratory disease; antiinflammatory; dermatological disease;
XX KW immunosuppressive; antibody.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Region 24..36
XX FT /note= "CDR (Complementarity-determining region)-H1"
XX FT Region 51..66
XX FT /note= "CDR (Complementarity-determining region)-H2"
XX FT Region 99..110
XX FT /note= "CDR (Complementarity-determining region)-H3"
XX XX
XX FN US2004259077-A1.
XX PD 23-DEC-2004.
XX PF 02-MAR-2004; 2004US-00791619.
XX XX 02-JUL-1997; 97US-0051554P.
XX PR 30-JUN-1998; 98US-00109207.
XX PD 17-NOV-2000; 2000US-00716028.
XX PF (GETH ) GENENTECH INC.
XX XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX PI WPI; 2005-038757/04.
XX DR
XX XX Treating an IgG-mediated disorder, e.g. asthma, allergic rhinitis,
XX PT eczema, urticaria, food allergies, or hypersensitivity, by administering
XX PT an anti-IgE antibody or its antigen-binding fragment.
XX XX
XX PS Disclosure; SEQ ID NO 12; 92pp; English.
XX XX The present invention relates to a method for treating an IgE-mediated
XX CC disorder. The method involves administering a therapeutical amount of an
XX CC anti-IgE antibody or its IgE binding fragment. The invention is useful
XX CC for treating an IgE-mediated disorder e.g. asthma, allergic rhinitis,
XX CC eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic
XX CC hypersensitivity. The present sequence is the human anti-IgE antibody
XX CC e26, e27 and e426 variable heavy chain protein.
XX SQ Sequence 114 AA;
XX Query Match 100.0%; Score 64; DB 9; Length 114;
XX Best Local Similarity 100.0%; Pred. No. 0.0083;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSITSGYSWN 11
DB |||||
26 GYSITSGYSWN 36

RESULT 10
ADW79890
ID ADW79890 standard; protein; 114 AA.
XX AC ADW79890;
XX DT 21-APR-2005 (first entry)
XX DE Anti-IgE antibody e26/e426/e25 heavy chain CDR domain fragment, SEQ ID 5.
XX XX
XX KW Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory;
XX KW Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma;
XX KW chronic obstructive pulmonary disease; respiratory disease;
XX KW pulmonary disease; cystic fibrosis; dyspnea; emphysema;
XX KW pulmonary hypertension; pulmonary fibrosis;
XX KW hyperresponsiveness of the airways; infectious diseases;
XX KW respiratory tract inflammation; chronic bronchitis;
XX KW respiratory distress syndrome; pain; allergic rhinitis; cancer;
XX KW immunoglobulin E; IgE; antibody; antibody therapy.
XX OS Synthetic.
XX XX
XX PN US2005026881-A1.
XX PN 03-FEB-2005.
XX PD
XX PF 29-OCT-2003; 2003US-00698073.
XX XX
XX PR 31-JUL-2003; 2003US-0492231P.
XX XX
XX PA (ROBI/) ROBINSON C B.
XX PA (BALL/) BALL H A.
XX XX
XX PI Robinson CB, Ball HA;
XX XX
XX DR WPI; 2005-161309/17.

```

XX Composition used for treating e.g. asthma, chronic obstructive pulmonary
PT disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and
PT cancer, comprises carrier, non-glucocorticoid steroids and anti-
PT immunoglobulin E antibody.
XX
XX Disclosure; SEQ ID NO 5; 62pp; English.
XX
XX The present invention relates to compositions comprising a carrier, a
XX first active agent comprising non-glucocorticoid steroids or their salts
XX and a second active agent comprising an anti-immunoglobulin E (IgE)
XX antibody effective to treat asthma, chronic obstructive pulmonary disease
XX or a respiratory or lung disease. The compositions are useful for
XX reducing the probability of or treating asthma and chronic obstructive
XX pulmonary disease. The compositions are also useful for treating
XX respiratory, lung/malignant disorder/condition such as asthma, chronic
XX obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema,
XX wheezing, pulmonary hypertension, pulmonary fibrosis, hyper-responsive
XX airways, increased adenosine or adenosine receptor levels, adenosine
XX hypersensitivity, infectious diseases, pulmonary bronchoconstriction,
XX respiratory tract inflammation or allergies, lung surfactant or
XX ubiquinone depletion, chronic bronchitis, bronchoconstriction, difficult
XX function, pulmonary vasoconstriction, impeded respiration, acute
XX respiratory distress syndrome, infantile respiratory distress syndrome, pain,
XX allergic rhinitis, cancer or chronic bronchitis, and for reducing levels
XX of/sensitivity to adenosine or adenosine receptors. The present sequence
XX is a humanized anti-IgE antibody CDR domain, used to illustrate the
XX invention.
XX
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 64; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYSITSGYSWN 11
DB 26 GYSITSGYSWN 36
|||||
RESULT 11
ADW79889
ID ADW79889 standard; protein; 114 AA.
XX
XX ADW79889;
XX
XX 21-APR-2005 (first entry)
XX
XX Anti-IgE antibody e27 heavy chain CDR domain fragment, SEQ ID 4.
XX
XX Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory;
XX Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma;
XX chronic obstructive pulmonary disease; respiratory disease;
XX pulmonary disease; cystic fibrosis; dyspnea; emphysema;
XX pulmonary hypertension; pulmonary fibrosis;
XX hyperresponsiveness of the airways; infectious diseases;
XX respiratory tract inflammation; chronic bronchitis;
XX respiratory distress syndrome; pain; allergic rhinitis; cancer;
XX immunoglobulin E; IgE; antibody; antibody therapy.
XX
XX Synthetic.
XX
XX US2005026881-A1.
XX
XX 03-FEB-2005.
XX
XX 29-OCT-2003; 2003US-00698073.
XX
XX 31-JUL-2003; 2003US-0492231P.
XX
XX (ROBI/) ROBINSON C B.

PA (BALL/) BALL H A.
XX Robinson CB, Ball HA;
XX WPI; 2005-161309/17.
XX
XX Composition used for treating e.g. asthma, chronic obstructive pulmonary
PT disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and
PT cancer, comprises carrier, non-glucocorticoid steroids and anti-
PT immunoglobulin E antibody.
XX
XX Disclosure; SEQ ID NO 4; 62pp; English.
XX
XX The present invention relates to compositions comprising a carrier, a
XX first active agent comprising non-glucocorticoid steroids or their salts
XX and a second active agent comprising an anti-immunoglobulin E (IgE)
XX antibody effective to treat asthma, chronic obstructive pulmonary disease
XX or a respiratory or lung disease. The compositions are useful for
XX reducing the probability of or treating asthma and chronic obstructive
XX pulmonary disease. The compositions are also useful for treating
XX respiratory, lung/malignant disorder/condition such as asthma, chronic
XX obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema,
XX wheezing, pulmonary hypertension, pulmonary fibrosis, hyper-responsive
XX airways, increased adenosine or adenosine receptor levels, adenosine
XX hypersensitivity, infectious diseases, pulmonary bronchoconstriction,
XX respiratory tract inflammation or allergies, lung surfactant or
XX ubiquinone depletion, chronic bronchitis, bronchoconstriction, difficult
XX breathing, impeded or obstructed lung airways, adenosine test for cardiac
XX function, pulmonary vasoconstriction, impeded respiration, acute
XX respiratory distress syndrome, infantile respiratory distress syndrome, pain,
XX allergic rhinitis, cancer or chronic bronchitis, and for reducing levels
XX of/sensitivity to adenosine or adenosine receptors. The present sequence
XX is a humanized anti-IgE antibody CDR domain, used to illustrate the
XX invention.
XX
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 64; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYSITSGYSWN 11
DB 26 GYSITSGYSWN 36
|||||
RESULT 12
AAO20095
ID AAO20095 standard; protein; 119 AA.
XX
XX AAO20095;
XX
XX 12-JUN-2002 (first entry)
XX
XX Protein encoded by a 357nt DNA sequence of the invention.
XX
XX Mouse monoclonal antibody; murine; surface antigen preS1 epitope;
XX hepatitis B virus.
XX
XX Unidentified.
XX
XX KR99008647-A.
XX
XX 05-FEB-1999.
XX
XX 02-JUL-1997; 97KR-00030694.
XX
XX 02-JUL-1997; 97KR-00030694.
XX
XX (KORE-) KOREA RES INST CHEM TECHNOLOGY.
XX
XX Hong HJ, Ryoo CJ;


```

XX 17-APR-2001 (first entry)
XX Variable heavy chain sequence of MaE11 SEQ ID 2.
XX
XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
XX antinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX conjunctivitis; eczema; urticaria; food allergy.
XX
XX Mus musculus.
XX
XX US6172213-B1.
XX
XX 09-JAN-2001.
XX
XX 30-JUN-1998; 98US-00109207.
XX
XX 02-JUL-1997; 97US-0051554P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX WPI; 2001-122353/13.
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX properties, produced by substituting aspartyl residues in unimproved
XX immunoglobulin E prone to isomerization by other residues by affinity
XX maturation with phase display.
XX
XX Example 2; Fig 1; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody with
XX improved anti-IgE antibody activity. The antibody has improved action due
XX to a process comprising, a) identifying aspartyl residues prone to
XX isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX substituting alternative residues to create candidate molecules, and c)
XX selecting those candidate molecules which display affinity against the
XX target molecule. Use of the antibody results in antiasthmatic;
XX antiallergic; ophthalmological; dermatological and antiinflammatory
XX activity. The antibodies are useful for treating IgE-mediated disorders
XX such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
XX food allergies. The mutant antibodies produced by the above mentioned
XX nucleic acids may also be used as affinity purification agents and in
XX diagnostic assays for detecting the expression of an antigen of interest
XX in specific cell, tissues or serum. Amino acid sequences AAB76936-
XX AAB76960 represent fragments of anti-IgE antibodies of the invention.
XX Polynucleotide sequence AAF69253 represents an expression plasmid used in
XX the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
XX used in the generation of affinity improved anti-IgE antibodies
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 64; DB 4; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.0088;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYSITSGYSWN 11
XX |||||
XX Db 26 GYSITSGYSWN 36
XX
XX Search completed: April 25, 2006, 06:15:02
XX Job time : 60.7358 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:15:41 ; Search time 9.33962 Seconds
(without alignments)
113.322 Million cell updates/sec

Title: US-10-764-428-19
Perfect score: 64
Sequence: 1 GYSITSGYSWN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	92.2	116	1 HVMS1B	Ig heavy chain pre
2	58	90.6	104	2 S26467	Ig heavy chain v r
3	58	90.6	116	1 HVMS31	Ig heavy chain pre
4	58	90.6	119	2 E25114	Ig heavy chain v r
5	58	90.6	137	1 AVMS35	Ig heavy chain pre
6	56	87.5	120	2 A25114	Ig heavy chain v r
7	56	87.5	149	2 S30752	Ig heavy chain pre
8	54	84.4	106	2 S59639	Ig heavy chain v r
9	54	84.4	106	2 S26464	Ig heavy chain v r
10	54	84.4	114	2 T01262	Ig heavy chain v r
11	54	84.4	116	2 S38718	Ig heavy chain v r
12	53	82.8	59	2 S36379	Ig heavy chain v r
13	53	82.8	117	2 I28195	Ig heavy chain v r
14	52	81.2	115	2 F25114	Ig heavy chain v r
15	52	81.2	121	2 S37200	Ig heavy chain v r
16	50	78.1	143	2 S07454	Ig heavy chain v r
17	49	76.6	135	2 F20100	Ig heavy chain pre
18	48	75.0	98	2 S26902	Ig heavy chain v r
19	48	75.0	98	2 S12421	Ig heavy chain v r
20	48	75.0	119	2 D25114	Ig heavy chain v r
21	48	75.0	123	2 S30530	Ig heavy chain v r
22	48	75.0	130	2 S31873	Ig heavy chain v r
23	48	75.0	140	2 A24770	hypothetical hybri
24	47	73.4	348	2 E70009	conserved hypochet
25	46	71.9	139	2 C53285	Ig heavy chain v a
26	45	70.3	134	2 B24672	Ig heavy chain pre
27	44	68.8	119	2 C25114	Ig heavy chain v r
28	43	67.2	91	2 S13689	Ig heavy chain v r
29	43	67.2	110	2 S13688	Ig heavy chain v r

30	43	67.2	111	2 S13687	Ig heavy chain v r
31	43	67.2	112	2 S13686	Ig heavy chain v r
32	43	67.2	112	2 S13685	Ig heavy chain v r
33	43	67.2	136	2 S07637	Ig heavy chain v r
34	42	65.6	303	2 H35068	apolipoprotein H-r
35	42	65.6	320	2 G75284	probable potassium
36	42	65.6	446	2 G70510	probable oxidoredu
37	42	65.6	452	2 A35068	complement factor
38	42	65.6	1234	1 NEMSH	complement factor
39	41	64.1	103	2 E70638	hypothetical prote
40	40	62.5	289	2 A84030	hypothetical prote
41	40	62.5	471	2 A25245	hypothetical prote
42	40	62.5	621	2 A71221	aldehyde-ferredoxi
43	40	62.5	1050	2 JC7889	heparinase (RC 3.2
44	39.5	61.7	94	2 S26461	Ig heavy chain v r
45	39.5	61.7	100	2 S14485	Ig heavy chain v r

ALIGNMENTS

RESULT 1

HVMS1B

Ig heavy chain precursor V region (IB43) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C:Accession: J70508

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J70501; MUID:89279149; PMID:2499654

A:Accession: J70508

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-116 <LEV>

A:Cross-references: UNIPROT:P18532; UNIPARC:UPI00000278E1

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH3660 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-116/Product: Ig heavy chain V region (IB43) #status predicted <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 92.2%; Score 59; DB 1; Length 116;
Best Local Similarity 90.9%; Pred. No. 0.007;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
DB 44 GYSITSGYSWH 54

RESULT 2

S26467

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26467

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26467

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <KAV>

A:Cross-references: UNIPARC:UPI0000115F5F; EMBL:X59105; NID:g51939; PIDN:CAA41831.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:6-89/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 58; DB 2; Length 104;
Best Local Similarity 90.9%; Pred. No. 0.0092;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||

Db 17 GYSITSGYWN 27

RESULT 3

HWS31 Ig heavy chain precursor V region (M315) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C:Accession: J70509

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J70501; MUID:89279149; PMID:2499654

A:Accession: J70509

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-116 <LEV>

A:CROSS-references: UNIPROT:P18531; UNIPARC:UPI00000278E0

A:Experimental source: strain BALB/cJ

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-116/Product: Ig heavy chain V region (M315) #status predicted <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 58; DB 1; Length 116;

Best Local Similarity 90.9%; Pred. No. 0.01;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11

|||||

Db 44 GYSITSGYWN 54

RESULT 4

E25114

Ig heavy chain V region (HP25) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000

C:Accession: E25114

R:Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Fougereau, M.

EMBO J. 4, 3681-3688, 1985

A:Title: The idiotypic network and the internal image: possible regulation of a germ-line

A:Reference number: A91028; MUID:86136012; PMID:3937730

A:Accession: E25114

A:Molecule type: mRNA

A:Residues: 1-119 <OLL>

A:CROSS-references: UNIPARC:UPI0000115D24; GB:X03378; NID:952007; PIDN:CAA27095.1; PID:9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 58; DB 2; Length 119;

Best Local Similarity 90.9%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11

|||||

Db 26 GYSITSGYWN 36

RESULT 5

AW535

Ig heavy chain precursor V region (MOPC 315) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: PL0102; S03262; A93814; A91462; A93787; S23599

R:Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.

Mol. Immunol. 26, 431-434, 1989

A:Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.

A:Reference number: PL0102; MUID:89238351; PMID:2497341

A:Accession: PL0102

A:Molecule type: mRNA

A:Residues: 1-137 <RIN>

A:CROSS-references: UNIPROT:P01822; UNIPARC:UPI000002727B; GB:M27638; NID:9602706; PIDN:

A:Experimental source: strain MOPC 315

R:Rinfret, A.; Dorrington, K.J.; Klein, M.

submitted to the EMBL Data Library, June 1988

A:Reference number: S03262

A:Accession: S03262

A:Molecule type: DNA

A:Residues: 1-15,'G',16-137 <RI2>

A:CROSS-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:951760; PIDN:CAA30727.1; PID:

R:Jilka, R.L.; Pestka, S.

Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977

A:Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin h

A:Reference number: A93814; MUID:78094475; PMID:414225

A:Accession: A93814

A:Molecule type: protein

A:Residues: 1-14,'H',16-31 <JIL>

A:CROSS-references: UNIPARC:UPI000017373E

A:Note: the authors translated mRNA in vitro to obtain the precursor protein

R:Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.

Fed. Proc. 38, 1839-1845, 1979

A:Title: Structure and function of immunoglobulin genes and precursors.

A:Reference number: A91462; MUID:79148758; PMID:428562

A:Accession: A91462

A:Molecule type: protein

A:Residues: 1,'X',3-11,'X',14-21 <SCH>

A:CROSS-references: UNIPARC:UPI000017373F

A:Note: the authors translated mRNA in vitro to obtain the precursor protein

R:Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.

Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974

A:Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse

A:Reference number: A93787; MUID:74170779; PMID:4524622

A:Accession: A93787

A:Molecule type: protein

A:Residues: 19-52,'K',53-75,'BYGB',80-101,'D',103-106,'ZB',109-122,124-137 <FRA>

A:CROSS-references: UNIPARC:UPI0000173740

R:Hood, L.; Margolies, M.; Givol, D.; Zakut, R.

unpublished results, cited by Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wrig

A:Reference number: A94484

A:Contents: annotation; revision to residue 53

R:Chadale, C.; Hook, L.B.; Givol, D.; Ricca, G.A.

Mol. Immunol. 29, 21-30, 1992

A:Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315

A:Reference number: S23599; MUID:92114886; PMID:1731188

A:Accession: S23599

A:Molecule type: mRNA

A:Residues: 19-137 <CHE>

A:CROSS-references: UNIPARC:UPI0000113794; EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID:

C:Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe

C:Genetics:

F:19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 58; DB 1; Length 137;

Best Local Similarity 90.9%; Pred. No. 0.012;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11

|||||

Db 44 GYSITSGYFWN 54

RESULT 6

A25114

Ig heavy chain V region (HP22, HP27) - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
 C:Accession: A25114
 R:Ollier, P.; Rocca-Serra, J.; Somme, G.; There, J.; Fougereau, M.
 ENBO J. 4, 3681-3688, 1985
 A:Title: The idiotypic network and the internal image: possible regulation of a germ-line
 A:Reference number: A91028; MUID:86136012; PMID:3937730
 A:Accession: A25114
 A:Molecule type: mRNA
 A:Residues: 1-120 <OLL>
 A:Cross-references: UNIPARC:UPI0000115D15; GB:X03374; NID:G51983; PIDN:CAA27071.1; PID:8
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 56; DB 2; Length 120;
 Best Local Similarity 81.8%; Pred. No. 0.023;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 ||||| :||
 Db 26 GYSITRGYNWN 36

RESULT 7
 S30752
 Ig heavy chain precursor V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
 C:Accession: S30752
 R:Grant, P.J.; Levin, S.D.; Gilbert, T.; Kindavogel, W.
 Nucleic Acids Res. 15, 5496, 1987
 A:Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
 A:Reference number: S30751; MUID:87260030; PMID:3601683
 A:Accession: S30752
 A:Molecule type: mRNA
 A:Residues: 1-149 <GRA>
 A:Cross-references: UNIPARC:UPI0000115D92; EMBL:X05878; NID:G52526; PIDN:CAA29302.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:33-116/Domain: immunoglobulin homology <IMM>
 F:138-149/Domain: C region (C-gamma 2b) (fragment) #status predicted <CR>

Query Match 87.5%; Score 56; DB 2; Length 149;
 Best Local Similarity 81.8%; Pred. No. 0.029;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 ||||| :||
 Db 44 GYSITSGYTW 54

RESULT 8
 S59639
 Ig heavy chain V region N10 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
 C:Accession: S59639
 R:Bosart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
 J. Mol. Biol. 253, 559-575, 1995
 A:Title: The crystal structure of the antibody N10-staphylococcal nuclease complex at 2.
 A:Reference number: S59639; MUID:96068846; PMID:7473734
 A:Accession: S59639
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-106 <BOS>
 A:Cross-references: UNIPARC:UPI0000176905; EMBL:U25121
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 54; DB 2; Length 106;
 Best Local Similarity 81.8%; Pred. No. 0.044;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 ||||| :||
 Db 19 GYSITSDYAWN 29

RESULT 9
 S26464
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26464
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26464
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-106 <KAV>
 A:Cross-references: UNIPARC:UPI0000115F68; EMBL:X59114; NID:G51926; PIDN:CAA41840.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 54; DB 2; Length 106;
 Best Local Similarity 81.8%; Pred. No. 0.044;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 ||||| :||
 Db 14 GYSITSDYAWN 24

RESULT 10
 T01262
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01262
 R:Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
 AIDS Res. Hum. Retroviruses 9, 41-49, 1993
 A:Title: Variable region gene utilization and mutation in a group of neutralizing murin
 A:Reference number: Z14285; MUID:93152285; PMID:7678971
 A:Accession: T01262
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-114 <PIR>
 A:Cross-references: UNIPARC:UPI0000117638; EMBL:S54194; NID:G264864; PIDN:AAB25246.2; P
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 54; DB 2; Length 114;
 Best Local Similarity 81.8%; Pred. No. 0.047;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 ||||| :||
 Db 26 GYSITSDYAWN 36

RESULT 11
 S38718
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S38718
 R:Cimanis, A.Y.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S38713
 A:Accession: S38718
 A:Status: preliminary
 A:Molecule type: mRNA

A;Residues: 1-116 <C1M>
A;Cross-references: UNIPARC:UPI0000117542; EMBL:X76018; NID:g416102; PIDN:CAAS3605.1; PID:9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 54; DB 2; Length 116;
Best Local Similarity 81.8%; Pred. No. 0.048; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
||||| :||
Db 26 GYSITSDYAWN 36

RESULT 12
S36379
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
C;Accession: S36379; S33394
R;Ansell, K.H.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36376
A;Accession: S36379
A;Molecule type: mRNA
A;Residues: 1-59 <ANS>
A;Cross-references: UNIPARC:UPI00001161F; EMBL:X73007; NID:g295874; PIDN:CAAS1494.1; PID:9
R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A;Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes used
A;Reference number: S33391; MUID:93122092; PMID:8419173
A;Accession: S33394
A;Molecule type: mRNA
A;Residues: 1-31,33-39 <KET>
A;Cross-references: UNIPARC:UPI00001768F4; EMBL:X73007
A;Experimental source: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-59/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 82.8%; Score 53; DB 2; Length 59;
Best Local Similarity 81.8%; Pred. No. 0.035; 2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
||||| :||
Db 24 GYSITSDYAWN 34

RESULT 13
I28195
Ig heavy chain V region (anti-haloperidol antibody D) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: I28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: I28195
A;Molecule type: mRNA
A;Residues: 1-117 <SHE>
A;Cross-references: UNIPARC:UPI0000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID:9
C;Note: the authors translated the codon AAC for residue 61 as Thr, and did not translat
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 53; DB 2; Length 117;
Best Local Similarity 81.8%; Pred. No. 0.071; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
||||| :||
Db 26 GYSITSDYAWN 36

RESULT 14

F25114

Ig heavy chain V region (HP12) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000

C;Accession: F25114

R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

EMBO J. 4, 3681-3688, 1985

A;Title: The idiotypic network and the internal image: possible regulation of a germ-line

A;Reference number: A91028; MUID:86136012; PMID:3937730

A;Accession: F25114

A;Molecule type: mRNA

A;Residues: 1-115 <OLL>

A;Cross-references: UNIPARC:UPI0000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:9

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 52; DB 2; Length 115;

Best Local Similarity 81.8%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11

||||| :||

Db 26 GYSITSDYAWN 36

RESULT 15

S37200

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S37200

R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.

submitted to the EMBL Data Library, August 1993

A;Description: Production and cloning of TMV-specific monoclonal antibodies.

A;Reference number: S37200

A;Accession: S37200

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-121 <FIS>

A;Cross-references: UNIPARC:UPI00001161AC; EMBL:X74587; NID:g402639; PID:g402640

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 52; DB 2; Length 121;

Best Local Similarity 81.8%; Pred. No. 0.11; 2; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11

||||| :||

Db 26 GYSITSDYAWN 36

Search completed: April 25, 2006, 06:26:10

Job time : 11.3396 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:44 ; Search time 58.7358 Seconds
(without alignments)
132.131 Million cell updates/sec

Title: US-10-764-428-19
Perfect score: 64
Sequence: 1 GYSTSGYSWN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	92.2	116	1 HV61_MOUSE	P18532 mus musculus
2	58	90.6	98	2 Q53VQ4_MOUSE	Q53VQ4 mus musculus
3	58	90.6	116	1 HV60_MOUSE	P18531 mus musculus
4	58	90.6	119	2 Q53VQ5_MOUSE	Q53VQ5 mus musculus
5	58	90.6	137	1 HV46_MOUSE	P01822 mus musculus
6	58	90.6	479	2 Q99M22_MOUSE	Q99M22 mus musculus
7	56	87.5	98	2 Q53VR6_MOUSE	Q53VR6 mus musculus
8	56	87.5	120	2 Q53VR7_MOUSE	Q53VR7 mus musculus
9	55	85.9	483	2 Q5U413_MOUSE	Q5U413 mus musculus
10	53	82.8	590	2 Q569B8_RAT	Q569B8 rattus norv
11	52	81.2	98	2 Q53VQ0_MOUSE	Q53VQ0 mus musculus
12	52	81.2	115	2 Q53VQ1_MOUSE	Q53VQ1 mus musculus
13	48	75.0	98	2 Q53VQ8_MOUSE	Q53VQ8 mus musculus
14	48	75.0	119	2 Q53VQ9_MOUSE	Q53VQ9 mus musculus
15	47	73.4	348	2 Q05254_BACSU	Q05254 bacillus eu
16	45	70.3	246	2 Q4MZP1_THEPA	Q4MZP1 theileria p
17	45	70.3	610	2 Q4J916_SULAC	Q4J916 sulfolobus
18	44	68.8	98	2 Q53VR2_MOUSE	Q53VR2 mus musculus
19	44	68.8	119	2 Q53VR3_MOUSE	Q53VR3 mus musculus
20	44	68.8	512	2 Q8WQK6_PLAFA	Q8WQK6 plasmodium
21	44	68.8	512	2 Q812G4_PLAF7	Q812G4 plasmodium
22	43	67.2	136	2 Q6LBQ5_MOUSE	Q6LBQ5 mus musculus
23	43	67.2	257	2 Q85V77_9CAUD	Q85V77 mycobacteri
24	42	65.6	277	2 Q84CZ0_RHILV	Q84CZ0 rhizobium l
25	42	65.6	303	2 Q61405_MOUSE	Q61405 mus musculus
26	42	65.6	320	2 Q9RRZ3_DEIRA	Q9RRZ3 deinococcus
27	42	65.6	332	2 Q4LDF6_MOUSE	Q4LDF6 mus musculus
28	42	65.6	446	2 Q7D7Z7_MYCTU	Q7D7Z7 mycobacteri
29	42	65.6	446	2 Q33177_MYCTU	Q33177 mycobacteri
30	42	65.6	446	2 Q7TZK4_MYCBO	Q7TZK4 mycobacteri
31	42	65.6	452	2 Q61407_MOUSE	Q61407 mus musculus

Q5b8t9 aspergillus
Q8r018 mus musculus
P06909 mus musculus
Q6nzK3 mus musculus
Q7tZ79 mycobacteri
P95261 mycobacteri
Q4hw71 gibberella
Q4kdel pseudomonas
Q51u19 magnaporthe
Q8ga49 escherichia
Q4phr5 ustilago ma
Q55u15 cryptococcu
Q5kic6 cryptococcu
Q610n5 picophyllus

32 42 65.6 498 2 Q5B8T9_EMENI
33 42 65.6 509 2 Q8R018_MOUSE
34 42 65.6 1234 1 CFAH_MOUSE
35 42 65.6 1234 2 Q6NZK3_MOUSE
36 41 64.1 103 2 Q7TZ79_MYCBO
37 41 64.1 103 2 P95261_MYCTU
38 41 64.1 285 2 Q4HW71_GIBZE
39 41 64.1 287 2 Q4KDB1_PSEFS
40 41 64.1 690 2 Q51UI9_MAGGR
41 41 64.1 835 2 Q8GA49_ECOLI
42 41 64.1 1438 2 Q4PHR5_USTMA
43 40.5 63.3 252 2 Q55U15_CRYNE
44 40.5 63.3 252 2 Q5KIC6_CRYNE
45 40 62.5 205 2 Q610N5_PICTO

ALIGNMENTS

RESULT 1

ID HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
DS Mus musculus (Mouse)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAALB/cu;
RX MEDLINE=89279149; PubMed=2499854; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC PIR; JT0508; HVMS1B.
DR PDB; 1KCS; X-ray; H=25-116.
DR PDB; 1KCV; X-ray; H=25-116.
DR Ensembl; ENSMUSG0000006162; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 Ig heavy chain V region 1B43.
FT REGION 19 48 Framework-1.
FT REGION 49 53 Complementarity-determining-1.
FT REGION 54 67 Framework-2.
FT REGION 68 84 Complementarity-determining-2.
FT REGION 85 116 Framework-3.
FT DISULFID 40 114 By similarity.
FT NON_TER 116 116
FT STRAND 21 25
FT STRAND 29 30
FT TURN 32 33
FT TURN 36 43
FT TURN 47 49
FT STRAND 52 58
FT TURN 60 61

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PT STRAND 64 71
FT TURN 72 73
FT STRAND 76 78
FT TURN 80 85
FT STRAND 86 91
FT TURN 92 95
FT STRAND 96 101
FT HELIX 106 108
FT STRAND 110 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 92.2%; Score 59; DB 1; Length 116;
Best Local Similarity 90.9%; Pred. No. 0.043;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 44 GYSITSGYSWH 54

RESULT 2
Q53VQ4 MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53VQ4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]

RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27096.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11202 MW; 4049CF8C7EB8AAE0 CRC64;

Query Match 90.6%; Score 58; DB 2; Length 98;
Best Local Similarity 90.9%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYWN 36

RESULT 3
HV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]

RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27096.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11202 MW; 4049CF8C7EB8AAE0 CRC64;

Query Match 90.6%; Score 58; DB 1; Length 116;
Best Local Similarity 90.9%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 44 GYSITSGYWN 54

RESULT 4
Q53VQ5 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]

RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27095.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;
```

Query Match 90.6%; Score 58; DB 2; Length 119;
 Best Local Similarity 90.9%; Pred. No. 0.065; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 DB 26 GYSITSGYWN 36

RESULT 5
 HV46 MOUSE STANDARD; PRT; 137 AA.
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region MOPC 315 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
 segment.";
 RL Mol. Immunol. 26:431-434(1989).
 RN [2]
 RP PROTEIN SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Peatka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP PROTEIN SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors.";
 RL Fed. Proc. 38:1839-1845(1979).
 RN [4]
 RP PROTEIN SEQUENCE OF 19-136.
 RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
 RT "Amino-acid sequence of the variable region of the heavy (alpha) chain
 of a mouse myeloma protein with anti-baptin activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP SEQUENCE REVISION TO 53.
 RX MEDLINE=77244979; PubMed=268248;
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 RT Unpublished results, cited by:
 RL Fadlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC C-1 MISCELLANEOUS: This alpha chain was isolated from a myeloma
 protein that has anti-dinitrophenyl activity.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC ENBL; M27638; AAA61337.1; -; Genomic_DNA.
 DR ENBL; X07880; CAA30727.1; -; Genomic_DNA.
 DR PIR; P0102; AVMS35.
 DR HSSP; P01820; 1G7J.
 DR SNR; P01822; 20-137.
 DR Ensembl; ENSMUSG0000057048; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.

SMART; SM00406; IGV; 1.
 PROSITE; PS00835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137
 FT REGION 19 48
 FT REGION 49 54
 FT REGION 55 68
 FT REGION 69 84
 FT REGION 85 116
 FT REGION 117 126
 FT REGION 127 137
 FT DISULFID 40 114
 FT CONFLICT 15 15
 FT CONFLICT 15 15
 FT CONFLICT 77 78
 FT CONFLICT 102 102
 FT CONFLICT 123 123
 FT NON_TER 137 137
 SQ SEQUENCE 137 AA; 15399 MW; PB3828304C2B81DC CRC64;

Query Match 90.6%; Score 58; DB 1; Length 137;
 Best Local Similarity 90.9%; Pred. No. 0.075; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 DB 44 GYSITSGYFWN 54

RESULT 6
 Q99M22 MOUSE
 ID Q99M22_MOUSE PRELIMINARY; PRT; 479 AA.
 AC Q99M22;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE LOC238447 protein.
 GN Name=LOC238447;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RG NIH MGC Project;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002091; AA02091.1; -; mRNA.
 DR HSP; P01820; IG7J.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 90.6%; Score 58; DB 2; Length 479;
 Best Local Similarity 90.9%; Pred. No. 0.29;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 44 GYSITSGYWN 54

RESULT 7
 Q53VR6 MOUSE
 ID Q53VR6 MOUSE PRELIMINARY; PRT; 98 AA.
 AC Q53VR6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE VH-region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 FT "The idiotypic network and the internal image: possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.

RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03375; CAA27078.1; -; mRNA.
 DR EMBL; X03374; CAA27072.1; -; mRNA.
 FT NON_TER 1 1
 FT NON_TER 98 98
 SQ SEQUENCE 98 AA; 11255 MW; EBC71A2F8F5FD60 CRC64;

Query Match 87.5%; Score 56; DB 2; Length 98;
 Best Local Similarity 81.8%; Pred. No. 0.11;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 26 GYSITRGYWN 36

RESULT 8
 Q53VR7 MOUSE
 ID Q53VR7 MOUSE PRELIMINARY; PRT; 120 AA.
 AC Q53VR7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE VH-DH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 FT "The idiotypic network and the internal image: possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03375; CAA27077.1; -; mRNA.
 DR EMBL; X03374; CAA27071.1; -; mRNA.
 FT NON_TER 1 1
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13892 MW; 013452306EBA3BE CRC64;

Query Match 87.5%; Score 56; DB 2; Length 120;
 Best Local Similarity 81.8%; Pred. No. 0.14;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
 |||||
 Db 26 GYSITRGYWN 36

RESULT 9
 Q5U413 MOUSE
 ID Q5U413 MOUSE PRELIMINARY; PRT; 483 AA.
 AC Q5U413;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE LOC544903 protein.
 GN Name=LOC544903;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udén I.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN-FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC085312; AAH85312.1; -, mRNA.
 DR Ensembl; ENSMUSG00000054328; Mus musculus.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR InterPro; IPR003006; IG cl.
 DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 483 AA; 52714 MW; 7C372DA501A4A0D1 CRC64;

Query Match 85.9%; Score 55; DB 2; Length 483;
 Best Local Similarity 81.8%; Pred. No. 0.93;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 |||||
 DB 44 GYSITSGYGNH 54

RESULT 10
 Q56988 RAT PRELIMINARY; PRT; 590 AA.
 AC Q56988; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Similar to Igh-6 protein.
 GN Name=LOC299357;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092580; AAH92580.1; -, mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; CI-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
 SQ SEQUENCE 590 AA; 65088 MW; FAC77FFA82302304 CRC64;

Query Match 82.8%; Score 53; DB 2; Length 590;
 Best Local Similarity 81.8%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 |||||
 DB 42 GYSITSSYRNW 52

RESULT 11
 Q53VQ0 MOUSE PRELIMINARY; PRT; 98 AA.
 AC Q53VQ0; MEDLINE=86136012; PubMed=3937730;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE VH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
 RT "The idiotypic network and the internal image: possible regulation of
 RT a germ-line network by paucigenic encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system."
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03379; CAA27102.1; -, mRNA.
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11191 MW; B3585BB6F080616 CRC64;
 Query Match 81.2%; Score 52; DB 2; Length 98;
 Best Local Similarity 81.8%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
 |||||
 DB 26 GYSITSSYRNW 36

RESULT 12
 Q53VQ1 MOUSE PRELIMINARY; PRT; 115 AA.
 AC Q53VQ1; MEDLINE=86136012; PubMed=3937730;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE VH-D-JH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03379; CAA27101.1; -; mRNA.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;

Query Match 81.2%; Score 52; DB 2; Length 115;
Best Local Similarity 81.8%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
DB 26 GYSIISGYWN 36

RESULT 13
Q53V08 MOUSE
ID Q53V08_MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53V08.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03379; CAA27090.1; -; mRNA.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11191 MW; 5B21145E5DA368C6 CRC64;

Query Match 75.0%; Score 48; DB 2; Length 98;
Best Local Similarity 72.7%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
DB 26 GYSIISGYWS 36

RESULT 14
Q53V09 MOUSE
ID Q53V09_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53V09.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

```

```

DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03377; CAA27089.1; -; mRNA.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;

Query Match 75.0%; Score 48; DB 2; Length 119;
Best Local Similarity 72.7%; Pred. No. 3.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
DB 26 GYSIISGYWS 36

RESULT 15
O05254 BACSU
ID O05254_BACSU PRELIMINARY; PRT; 348 AA.
AC O05254; Q795M0;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein YufP.
GN Name=yufP; OrderedLocusNames=BSU31560;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RX MEDLINE=97419515; PubMed=9274030;
RA Oudega B., Koningsstein G., Rodrigues L., de Sales Ramon M.,
RA Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenecker T.;
RT "Analysis of the Bacillus subtilis genome: cloning and nucleotide
RT sequence of a 62 kb region between 275 degrees (rnb) and 284 degrees
RT (pai).";
RL Microbiology 143:2769-2774 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RA Oudega B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrali E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

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RA Hilbert H., Holesappel S., Hosono S., Hullo M.-F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Prescan B., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vasearotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
 RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein B.,
 RA Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."
 RL Nature 390:249-256(1997).
 DR EMBL; Z93937; CAB07938.1; -; Genomic_DNA.
 DR EMBL; Z99120; CAB15145.1; -; Genomic_DNA.
 DR PIR; E70009; E70009.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; F:transport; IEA.
 DR InterPro; IPR001851; Bac_inmem_transp.
 DR InterPro; IPR002229; RhesusRHD.
 DR Pfam; PF02653; BPD_transp_2; 1.
 DR PRINTS; PR00342; RhesusRHD.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 348 AA; 36843 MW; 960C3D451B483EC3 CRC64;

Query Match 73.4%; Score 47; DB 2; Length 348;
 Best Local Similarity 69.2%; Pred. No. 15;
 Matches 9; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 GYSITSGYS--WN 11
 Db |||: ||| ||
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Search completed: April 25, 2006, 06:24:35
 Job time : 61.7358 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:25:05 ; Search time 14.8396 Seconds
(without alignments)
61.284 Million cell updates/sec

Title: US-10-764-428-19

Perfect score: 64

Sequence: 1 GYSITSGYSWN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/PCITUS COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	64	100.0	114	1	US-08-887-352B-11
2	64	100.0	114	2	US-08-887-352B-12
3	64	100.0	114	1	US-09-109-207C-11
4	64	100.0	114	2	US-09-109-207C-12
5	64	100.0	114	2	US-09-296-005-11
6	64	100.0	114	2	US-09-296-005-12
7	64	100.0	114	2	US-09-920-171-11
8	64	100.0	114	2	US-09-920-171-12
9	64	100.0	114	2	US-09-716-028-11
10	64	100.0	114	2	US-09-716-028-12
11	64	100.0	114	2	US-10-113-996-11
12	64	100.0	114	2	US-10-113-996-12
13	64	100.0	121	1	US-08-887-352B-2
14	64	100.0	121	1	US-08-887-352B-3
15	64	100.0	121	2	US-09-109-207C-2
16	64	100.0	121	2	US-09-109-207C-3
17	64	100.0	121	2	US-09-296-005-2
18	64	100.0	121	2	US-09-296-005-3
19	64	100.0	121	2	US-09-920-171-2
20	64	100.0	121	2	US-09-920-171-3
21	64	100.0	121	2	US-09-716-028-2
22	64	100.0	121	2	US-09-716-028-3
23	64	100.0	121	2	US-10-113-996-2
24	64	100.0	121	2	US-10-113-996-3
25	64	100.0	134	2	US-08-466-151-3
26	64	100.0	134	2	US-08-466-163B-3
27	64	100.0	134	2	US-09-802-096-3

28	64	100.0	134	2	US-09-802-077-3	Sequence 3, Appl
29	64	100.0	134	2	US-09-925-179-3	Sequence 3, Appl
30	64	100.0	229	1	US-08-887-352B-20	Sequence 20, Appl
31	64	100.0	229	1	US-08-887-352B-21	Sequence 21, Appl
32	64	100.0	229	2	US-09-109-207C-20	Sequence 20, Appl
33	64	100.0	229	2	US-09-109-207C-21	Sequence 21, Appl
34	64	100.0	229	2	US-09-296-005-20	Sequence 20, Appl
35	64	100.0	229	2	US-09-296-005-21	Sequence 21, Appl
36	64	100.0	229	2	US-09-920-171-20	Sequence 20, Appl
37	64	100.0	229	2	US-09-920-171-21	Sequence 21, Appl
38	64	100.0	229	2	US-09-716-028-20	Sequence 20, Appl
39	64	100.0	229	2	US-09-716-028-21	Sequence 21, Appl
40	64	100.0	229	2	US-10-113-996-20	Sequence 20, Appl
41	64	100.0	229	2	US-10-113-996-21	Sequence 21, Appl
42	64	100.0	233	1	US-08-887-352B-25	Sequence 25, Appl
43	64	100.0	233	1	US-08-887-352B-26	Sequence 26, Appl
44	64	100.0	233	2	US-09-109-207C-25	Sequence 25, Appl
45	64	100.0	233	2	US-09-109-207C-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-08-887-352B-11

; Sequence 11, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; TYPE: Amino Acid

; LENGTH: 114 amino acids

; TOPOLOGY: Linear

; US-08-887-352B-11

Query Match 100.0%; Score 64; DB 1; Length 114;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11

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Db 26 GYSITSGYSWN 36

RESULT 2

US-08-887-352B-12

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; Sequence 12, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
;   Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/887,352B
;   FILING DATE: 03-Jul-1997
;   CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
;   NAME: Svoboda, Craig G.
;   REGISTRATION NUMBER: 39,044
;   REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1489
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 114 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
; US-08-887-352B-12

Query Match      100.0%; Score 64; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 3
US-09-109-207C-11
; Sequence 11, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 5
US-09-296-005-11
; Sequence 11, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123Clr
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-296-005-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 6
US-09-296-005-12
; Sequence 12, Application US/09296005
; Patent No. 6290957
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QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 4
US-09-109-207C-12
; Sequence 12, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-12

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 5
US-09-296-005-11
; Sequence 11, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123Clr
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-296-005-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
Db      26 GYSITSGYSWN 36

RESULT 6
US-09-296-005-12
; Sequence 12, Application US/09296005
; Patent No. 6290957
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; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-12

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 7
US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgB Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 8
US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgB Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-12

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 9
US-09-716-028-11
; Sequence 11, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 10
US-09-716-028-12
; Sequence 12, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
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; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-12

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 9
US-09-716-028-11
; Sequence 11, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-11

Query Match      100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
Db      26 GYSITSGYSWN 36

RESULT 10
US-09-716-028-12
; Sequence 12, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgB Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
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; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-12

Query Match 100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 11
US-10-113-996-11
; Sequence 12, Application US/10113996
; Patent No. 6761889
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123CJUS
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11

Query Match 100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 12
US-10-113-996-12
; Sequence 12, Application US/10113996
; Patent No. 6761889
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123CJUS
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005

; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12

Query Match 100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 13
US-08-887-352B-2
; Sequence 2, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-2

Query Match 100.0%; Score 64; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
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Db 26 GYSITSGYSWN 36

RESULT 14
US-08-887-352B-3
; Sequence 3, Application US/08887352B
; Patent No. 5994511

Job time : 15.8396 secs

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-3

Query Match 100.0%; Score 64; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 15
US-09-109-207C-2
Sequence 2, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Mus musculus
US-09-109-207C-2

Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:58:17 ; Search time 47.9434 Seconds
(without alignments)
95.866 Million cell updates/sec

Title: US-10-764-428-19
Perfect score: 64
Sequence: 1 GYSITSGYSWN 11

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64	100.0	11	5	US-10-764-428-19
2	64	100.0	114	3	US-09-920-171-11
3	64	100.0	114	3	US-09-920-171-12
4	64	100.0	114	4	US-10-113-996-11
5	64	100.0	114	4	US-10-113-996-12
6	64	100.0	114	5	US-10-791-619-11
7	64	100.0	114	5	US-10-791-619-12
8	64	100.0	114	5	US-10-698-073-4
9	64	100.0	114	5	US-10-698-073-5
10	64	100.0	121	3	US-09-920-171-2
11	64	100.0	121	3	US-09-920-171-3
12	64	100.0	121	4	US-10-113-996-2
13	64	100.0	121	4	US-10-113-996-3
14	64	100.0	121	5	US-10-791-619-2
15	64	100.0	121	5	US-10-791-619-3
16	64	100.0	134	3	US-09-802-077-3
17	64	100.0	134	3	US-09-802-096-3
18	64	100.0	134	3	US-09-925-179-3
19	64	100.0	134	5	US-10-968-237-3
20	64	100.0	229	3	US-09-920-171-20
21	64	100.0	229	3	US-09-920-171-21
22	64	100.0	229	4	US-10-113-996-20
23	64	100.0	229	4	US-10-113-996-21
24	64	100.0	229	5	US-10-791-619-20
25	64	100.0	229	5	US-10-791-619-21
26	64	100.0	229	5	US-10-698-073-13
27	64	100.0	229	5	US-10-698-073-14

Sequence 25, Appl
Sequence 26, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 14, Appl

28 64 100.0 233 3 US-09-920-171-25
29 64 100.0 233 3 US-09-920-171-26
30 64 100.0 233 4 US-10-113-996-25
31 64 100.0 233 4 US-10-113-996-26
32 64 100.0 233 5 US-10-791-619-25
33 64 100.0 233 5 US-10-791-619-26
34 64 100.0 233 5 US-10-698-073-18
35 64 100.0 233 5 US-10-698-073-19
36 64 100.0 248 3 US-09-920-171-22
37 64 100.0 248 3 US-09-920-171-23
38 64 100.0 248 4 US-10-113-996-22
39 64 100.0 248 4 US-10-113-996-23
40 64 100.0 248 5 US-10-791-619-22
41 64 100.0 248 5 US-10-791-619-23
42 64 100.0 248 5 US-10-698-073-15
43 64 100.0 248 5 US-10-698-073-16
44 64 100.0 450 5 US-10-698-073-11
45 64 100.0 451 3 US-09-920-171-14

ALIGNMENTS

RESULT 1

US-10-764-428-19
; Sequence 19, Application US/10764428
; Publication No. US20040229310A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
; TITLE OF INVENTION: YIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
; FILE REFERENCE: 11669.120USUI
; CURRENT APPLICATION NUMBER: US/10/764,428
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,484
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E25 VH HVR1 residues 26-35
US-10-764-428-19

Query Match 100.0%; Score 64; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11

DB 1 GYSITSGYSWN 11

RESULT 2

US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21

; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match 100.0%; Score 64; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
| | | | | | | | | |
Db 26 GYSITSGYSWN 36

RESULT 3
US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-12

Query Match 100.0%; Score 64; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
| | | | | | | | | |
Db 26 GYSITSGYSWN 36

RESULT 4
US-10-113-996-11
; Sequence 11, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11

Query Match 100.0%; Score 64; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
| | | | | | | | | |
Db 26 GYSITSGYSWN 36

RESULT 5
US-10-113-996-12
; Sequence 12, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12

Query Match 100.0%; Score 64; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSITSGYSWN 11
| | | | | | | | | |
Db 26 GYSITSGYSWN 36

RESULT 6
US-10-791-619-11
; Sequence 11, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123E1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial

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;
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-11
Query Match 100.0%; Score 64; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 7
US-10-791-619-12
; Sequence 12, Application US/10791619
; Publication No. US2004025907A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-12
Query Match 100.0%; Score 64; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 8
US-10-698-073-4
; Sequence 4, Application US/10698073
; Publication No. US20050026881A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.201
; CURRENT APPLICATION NUMBER: US/10/698,073
; CURRENT FILING DATE: 2003-10-26
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-5
Query Match 100.0%; Score 64; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 9
US-10-698-073-5
; Sequence 5, Application US/10698073
; Publication No. US20050026881A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.201
; CURRENT APPLICATION NUMBER: US/10/698,073
; CURRENT FILING DATE: 2003-10-26
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 5
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-5
Query Match 100.0%; Score 64; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 10
US-09-920-171-2
; Sequence 2, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
US-09-920-171-2
Query Match 100.0%; Score 64; DB 3; Length 121;
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Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 11
US-09-920-171-3
; Sequence 3, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F(ab) sequence derived from MAE11
US-09-920-171-3

Query Match 100.0%; Score 64; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 12
US-10-113-996-2
; Sequence 2, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-113-996-2

Query Match 100.0%; Score 64; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 13
US-10-113-996-3
; Sequence 3, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F(ab) sequence derived from MAE11
US-10-113-996-3

Query Match 100.0%; Score 64; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 14
US-10-791-619-2
; Sequence 2, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-791-619-2

Query Match 100.0%; Score 64; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 15

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US-10-791-619-3
; Sequence 3, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IGS Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-121
; OTHER INFORMATION: F(ab) sequence derived from MAE11
US-10-791-619-3

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Query Match      100.0%; Score 64; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYSITSGYSWN 11
        |||||
DB      26 GYSITSGYSWN 36

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Search completed: April 25, 2006, 07:08:45
Job time : 47.9434 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21 ; Search time 7.0566 Seconds
(without alignments)
68.593 Million cell updates/sec

Title: US-10-764-428-19
Perfect score: 64
Sequence: 1 GYSITSGYSWN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	98	7	US-11-084-554-10
2	64	100.0	98	7	US-11-136-250-10
3	64	100.0	114	6	US-10-923-327-4
4	64	100.0	114	6	US-10-923-327-5
5	64	100.0	121	7	US-11-208-422-48
6	64	100.0	121	7	US-11-208-422-50
7	64	100.0	121	7	US-11-208-422-52
8	64	100.0	229	6	US-10-923-327-13
9	64	100.0	229	6	US-10-923-327-14
10	64	100.0	233	6	US-10-923-327-18
11	64	100.0	233	6	US-10-923-327-19
12	64	100.0	451	6	US-10-923-327-7
13	64	100.0	451	6	US-10-923-327-9
14	64	100.0	451	6	US-10-923-327-11
15	64	100.0	451	7	US-11-208-422-20
16	64	100.0	451	7	US-11-208-422-21
17	64	100.0	451	7	US-11-208-422-22
18	64	100.0	451	7	US-11-012-353-70
19	58	90.6	118	6	US-10-512-184-34
20	58	90.6	371	6	US-10-512-184-71
21	58	90.6	626	6	US-10-512-184-49
22	55	85.9	118	7	US-11-009-939-22
23	54	84.4	117	7	US-11-012-353-69
24	54	84.4	117	7	US-11-012-353-75
25	54	84.4	117	7	US-11-012-353-79

26	54	84.4	121	6	US-10-946-836A-12	Sequence 12, Appl
27	54	84.4	121	6	US-10-988-207-12	Sequence 12, Appl
28	54	84.4	127	7	US-11-012-353-52	Sequence 52, Appl
29	54	84.4	135	7	US-11-012-353-77	Sequence 77, Appl
30	54	84.4	135	7	US-11-012-353-81	Sequence 81, Appl
31	52	81.2	248	6	US-10-923-327-15	Sequence 15, Appl
32	52	81.2	248	6	US-10-923-327-16	Sequence 16, Appl
33	50	78.1	117	7	US-11-012-353-83	Sequence 83, Appl
34	50	78.1	135	7	US-11-012-353-85	Sequence 74, Appl
35	49	76.6	98	7	US-11-012-353-74	Sequence 74, Appl
36	49	76.6	123	7	US-11-012-353-73	Sequence 73, Appl
37	48	75.0	98	7	US-11-054-669-44	Sequence 44, Appl
38	48	75.0	98	7	US-11-004-590-48	Sequence 48, Appl
39	48	75.0	117	7	US-11-012-353-162	Sequence 162, App
40	48	75.0	125	6	US-10-469-469-34	Sequence 34, Appl
41	48	75.0	140	6	US-10-469-469-36	Sequence 36, Appl
42	48	75.0	158	6	US-10-469-469-38	Sequence 38, Appl
43	48	75.0	162	6	US-10-469-469-40	Sequence 40, Appl
44	48	75.0	250	7	US-11-054-515-1548	Sequence 1548, Ap
45	48	75.0	250	7	US-11-266-444-1548	Sequence 1548, Ap

ALIGNMENTS

RESULT 1
US-11-084-554-10
; Sequence 10, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-10

Query Match 100.0%; Score 64; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSITSGYSWN 11
Db 26 GYSITSGYSWN 36

RESULT 2
US-11-136-250-10
; Sequence 10, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554

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; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-10

Query Match 100.0%; Score 64; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
   |||||
Db 26 GYSITSGYSWN 36

RESULT 3
US-10-923-327-4
; Sequence 4, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/35054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-923-327-4

Query Match 100.0%; Score 64; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
   |||||
Db 26 GYSITSGYSWN 36

RESULT 4
US-10-923-327-5
; Sequence 5, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/35054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-923-327-4

Query Match 100.0%; Score 64; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
   |||||
Db 26 GYSITSGYSWN 36

RESULT 5
US-11-208-422-48
; Sequence 48, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 48
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-48

Query Match 100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
   |||||
Db 26 GYSITSGYSWN 36

RESULT 6
US-11-208-422-50
; Sequence 50, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
```

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; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 50
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-50

Query Match      100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
DB      26 GYSITSGYSWN 36

RESULT 7
US-11-208-422-52
; Sequence 52, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marwin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 52
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-52

Query Match      100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
DB      26 GYSITSGYSWN 36

RESULT 8
US-10-923-327-13
; Sequence 13, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-ICE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
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; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 13
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-13

Query Match      100.0%; Score 64; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
DB      26 GYSITSGYSWN 36

RESULT 9
US-10-923-327-14
; Sequence 14, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-ICE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 14
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-14

Query Match      100.0%; Score 64; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSITSGYSWN 11
      |||||
DB      26 GYSITSGYSWN 36

RESULT 10
US-10-923-327-18
; Sequence 18, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
```

```

; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-18

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Query Match      100.0%; Score 64; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYSITSGYSWN 11
        |||||
DB      26 GYSITSGYSWN 36

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RESULT 11
US-10-923-327-19
; Sequence 19, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-19

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Query Match      100.0%; Score 64; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYSITSGYSWN 11
        |||||
DB      26 GYSITSGYSWN 36

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RESULT 12
US-10-923-327-7
; Sequence 7, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-7

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```

Query Match      100.0%; Score 64; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYSITSGYSWN 11
        |||||
DB      26 GYSITSGYSWN 36

```

```

RESULT 13
US-10-923-327-9
; Sequence 9, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 9
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-9

```

```

Query Match      100.0%; Score 64; DB 6; Length 451;

```

Best Local Similarity 100.0%; Pred. No. 0.0047; Score 64; DB 6; Length 451;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 14
US-10-923-327-11
; Sequence 11, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROBIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROBIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-11

Query Match 100.0%; Score 64; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

RESULT 15
US-11-208-422-20
; Sequence 20, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2159R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 20
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-20

Query Match 100.0%; Score 64; DB 7; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSITSGYSWN 11
|||||
Db 26 GYSITSGYSWN 36

Search completed: April 25, 2006, 07:10:00
Job time : 7.22327 secs

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OM protein - protein search, using sw model

Run on: April 25, 2006, 06:05:16 ; Search time 53.3962 Seconds
(without alignments)
82.286 Million cell updates/sec

Title: US-10-764-428-14

Perfect score: 58

Sequence: 1 GYFTNYGIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	ADQ90710	Adg90710 Anti-VEGF
2	58	100.0	118	AAW70684	Aaw70684 Anti-VEGF
3	58	100.0	118	AAW70680	Aaw70680 Anti-VEGF
4	58	100.0	118	AAB13383	Aab13383 Anti-VEGF
5	58	100.0	118	ABP61249	Abp61249 Humanised
6	58	100.0	118	ABP61253	Abp61253 Humanised
7	58	100.0	479	ADQ14132	Ado14132 Plasmid P
8	58	100.0	479	ADQ90732	Adg90732 Anti-VEGF
9	58	100.0	479	ADQ90732	Adg90729 Anti-VEGF
10	58	100.0	479	ADQ90731	Adg90731 Anti-VEGF
11	58	100.0	479	ADQ90731	Adg90731 Chimeric
12	57	98.3	120	ABR83196	ABr83196 Murine L1
13	57	98.3	120	ABR83194	ABr83194 Murine L1
14	57	98.3	120	ABR83198	ABr83198 Humanised
15	57	98.3	120	ADU26544	Adu26544 Chimeric
16	57	98.3	120	ADU26540	Adu26540 Mouse L1
17	57	98.3	120	ADU26548	Adu26548 Humanised
18	55	94.8	10	AAW70611	Aaw70611 Anti-VEGF
19	55	94.8	10	AAW70611	Aag90311 Anti-huma
20	55	94.8	10	ABP61180	Abp61180 Humanised
21	55	94.8	10	ABP61180	Adr89785 Anti-CD70
22	55	94.8	10	AEA40554	Aea40554 Anti-VEGF
23	55	94.8	10	AEA40550	Aea40550 Anti-VEGF
24	55	94.8	67	ADH62639	Adh62639 Mouse ant

RESULT 1

ADQ90710

ID ADQ90710 standard; peptide; 10 AA.

XX AC ADQ90710;

DT 21-OCT-2004 (first entry)

DE Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:14.

XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW anti-inflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti-vascular endothelial cell growth factor antibody; heavy chain; HVR1.
OS Homo sapiens.
OS Synthetic.

XX PN WO2004065417-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-US001844.

XX PR 23-JAN-2003; 2003US-0442484P.

XX PA (GETH) GENENTECH INC.

XX PI Simmons L;

XX DR WPI; 2004-562149/54.

XX Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

XX Claim 13; SEQ ID NO 14; 161pp; English.

XX The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

ALIGNMENTS

CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC (variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular
 CC endothelial cell growth factor) antibody, which is used in the
 CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
 |||||
 Db 1 GYFTNYGIN 10

RESULT 2

AAW70684
 ID AAW70684 standard; peptide; 118 AA.

AC AAW70684;

DT 27-JAN-1999 (first entry)

DE Anti-VEGF humanised antibody variable heavy domain of variant Y0238-3.

XX Heavy variable domain; murine; humanised antibody;
 XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 XX VEGF-induced angiogenesis; tumour; retinal disorder;
 XX age-related macular degeneration; diabetic retinopathy;
 XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006504.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 10B; 100pp; English.

XX The present sequence represents a variable heavy domain of an affinity-

CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 118 AA;

Query Match 100.0%; Score 58; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10

|||||

Db 26 GYFTNYGIN 35

RESULT 3

AAW70680

ID AAW70680 standard; peptide; 118 AA.

AC AAW70680;

DT 27-JAN-1999 (first entry)

DE Anti-VEGF humanised antibody variable heavy domain of variant Y0192.

XX Heavy variable domain; murine; humanised antibody;

XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX VEGF-induced angiogenesis; tumour; retinal disorder;

XX age-related macular degeneration; diabetic retinopathy;

XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006504.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT states, also related nucleic acid, vectors and transformed cells.

XX Example 3; Fig 9B; 100pp; English.

XX The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 118 AA;

Query Match 100.0%; Score 58; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFNYGIN 10
 |||||
 DB 26 GYTFNYGIN 35

RESULT 4
 AAB13383
 ID AAB13383 standard; protein; 118 AA.
 AC AAB13383;
 XX
 DT 21-NOV-2000 (first entry)
 XX
 DE Anti-VEGF antibody Y0238-3 heavy chain variable domain.
 XX
 KW Y0243-1; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KW antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 XX Region 26..35
 XX /label= CDR-H1
 XX Region 50..66
 XX /label= CDR-H2
 XX Region 70..79
 XX /label= CDR-7
 XX Region 99..112
 XX /label= CDR-H3
 XX
 XX WO200037502-A2.
 XX
 XX 29-JUN-2000.
 XX
 XX 09-DEC-1999; 99WO-US029475.
 XX
 XX 22-DEC-1998; 98US-00218481.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Van Bruggen N, Ferrara N;
 XX
 XX WPI; 2000-442646/38.
 XX
 XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 XX diabetes and chronic inflammation in a mammal, comprises administering a
 XX human vascular endothelial cell growth factor antagonist.
 XX
 XX Disclosure; Fig 14B; 60pp; English.
 XX
 XX The present sequence is the heavy chain variable region of the affinity
 XX matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 XX Y0238-3. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 XX be used to treat conditions characterised by undesirable excessive
 XX neovascularisation. Such conditions include tumours (especially solid
 XX ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 XX other retinopathies, retrolental fibroplasia, age-related macular
 XX degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 XX (including Grave's disease), corneal and other tissue transplantation,
 XX and chronic inflammation. Oedemas associated with tumours, strokes and
 XX head trauma, and ascites associated with malignancies, meigs' syndrome,
 XX lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 XX effusion, may also be treated. Monoclonal antibodies are generated in

CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay
 XX
 XX Sequence 118 AA;
 Query Match 100.0%; Score 58; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ

QY 1 GYTFNYGIN 10
 |||||
 DB 26 GYTFNYGIN 35

RESULT 5
 ABP61249
 ID ABP61249 standard; protein; 118 AA.
 XX
 AC ABP61249;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE Humanised anti-VEGF Y0192 antibody variable heavy domain.
 XX
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder; Y0192; heavy chain;
 KW variable domain.
 XX
 XX Homo sapiens.
 XX Mus sp.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Domain 26..35
 XX /label= CDR-H1
 XX Domain 50..66
 XX /label= CDR-H2
 XX Domain 70..79
 XX /label= CDR-7
 XX Domain 99..112
 XX /label= CDR-H3
 XX
 XX US2002032315-A1.
 XX
 XX 14-MAR-2002.
 XX
 XX 06-APR-1998; 98US-00056160.
 XX
 XX 06-AUG-1997; 97US-0054856P.
 XX
 XX (BACA/) BACA M.
 XX (WELL/) WELLS J A.
 XX (PRES/) PRESTA L G.
 XX (LOWM/) LOWMAN H B.
 XX (CHEN/) CHEN Y M.
 XX
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX
 XX WPI; 2002-517920/55.
 XX
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 XX mammal, particularly for treating tumor or retinal disorders.
 XX
 XX Example 3; Fig 9; 47pp; English.
 XX
 XX The present invention relates to humanised anti-VEGF (vascular
 XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 XX particularly those having a tumour or a retinal disorder e.g. intraocular
 XX neovascular disorders. The present sequence is an exemplary heavy chain

CC variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 58; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYTFNYGIN 10
Db 26 GYTFNYGIN 35
RESULT 6
ID ABP61253 standard; protein; 118 AA.
XX
AC ABP61253;
XX
DT 20-SEP-2002 (first entry)
XX
DE Humanised anti-VEGF Y0238-3 antibody variable heavy domain.
XX
KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KW retinal disorder; intraocular neovascular disorder; Y0238-3; heavy chain;
KW variable domain.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
FH Key Location/Qualifiers
FT Domain 26..35
FT /label= CDR-H1
FT Domain 50..66
FT /label= CDR-H2
FT Domain 70..79
FT /label= CDR-7
FT Domain 99..112
FT /label= CDR-H3
XX
PN US2002032315-A1.
XX
PD 14-MAR-2002.
XX
PF 06-APR-1998; 98US-00056160.
XX
PR 06-AUG-1997; 97US-0054856P.
XX
PA (BACA/) BACA M.
PA (WELL/) WELLS J A.
PA (PRES/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
WPI; 2002-517920/55.
XX
PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX
PS Example 3; Fig 10; 47pp; English.
XX
CC The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention

XX
SQ Sequence 118 AA;
Query Match 100.0%; Score 58; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYTFNYGIN 10
Db 26 GYTFNYGIN 35
RESULT 7
ID ADO14132 standard; protein; 479 AA.
XX
AC ADO14132;
XX
DT 12-AUG-2004 (first entry)
XX
DE Plasmid pXVGL1VNERK expression cassette heavy chain protein SEQ ID NO:12.
XX
KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
KW expression cassette; plasmid pXVGL1VNERK; anti-VEGF heavy chain.
XX
OS Synthetic.
XX
WO2004042017-A2.
XX
PN WO2004042017-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034610.
XX
PR 31-OCT-2002; 2002US-0422952P.
XX
PA (GBTH) GENENTECH INC.
XX
PI Reilly D, Yansura DG;
XX
WPI; 2004-390607/36.
XX
DR N-PSDB; ADO14130.
XX
PT New antibody comprising a variant heavy chain hinge region incapable of
PT inter-heavy chain disulfide linkage, useful for treating, preventing,
PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
PT immune disorder.
XX
PS Example 1; SEQ ID NO 12; 124pp; English.
XX
CC The present invention describes an antibody comprising a variant heavy
CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
CC (2) an immunoconjugate comprising the antibody conjugated with a
CC heterologous moiety; (3) a composition comprising the antibody or
CC immunoconjugate, and carrier; (4) an article of manufacture comprising
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunoconjugate; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytostatic and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunoconjugate and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumour, cancer or immune disorder. The present sequence
CC represents the anti-VEGF heavy chain from the expression cassette of
CC plasmid pXVGL1VNERK, which is used in the exemplification of the present
CC invention.

SQ Sequence 479 AA;
 Query Match 100.0%; Score 58; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
 |||||
 Db 49 GYFTFTNYGIN 58

RESULT 8
 ADQ90737
 ID ADQ90737 standard; protein; 479 AA.
 XX AC ADQ90737;
 XX DT 21-OCT-2004 (first entry)
 XX DE Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:21.
 XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO2004065417-A2.
 XX 05-AUG-2004.
 XX 23-JAN-2004; 2004WO-US001844.
 XX 23-JAN-2003; 2003US-0442484P.
 XX (GETH) GENENTECH INC.
 XX Simmons L;
 XX WPI; 2004-562149/54.
 DR N-PSDB; ADQ90722.
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX Example 7; SEQ ID NO 27; 161pp; English.
 PS The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be

CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 XX Sequence 479 AA;
 Query Match 100.0%; Score 58; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
 |||||
 Db 49 GYFTFTNYGIN 58

RESULT 9
 ADQ90732
 ID ADQ90732 standard; protein; 479 AA.
 XX AC ADQ90732;
 XX DT 21-OCT-2004 (first entry)
 XX DE Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:11.
 XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO2004065417-A2.
 XX 05-AUG-2004.
 XX 23-JAN-2004; 2004WO-US001844.
 XX 23-JAN-2003; 2003US-0442484P.
 XX (GETH) GENENTECH INC.
 XX Simmons L;
 XX WPI; 2004-562149/54.
 DR N-PSDB; ADQ90706.
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX Example 2; SEQ ID NO 11; 161pp; English.
 PS The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen

CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 479 AA;

Query Match 100.0%; Score 58; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.56; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
 |||||
 Db 49 GYFTFTNYGIN 58

RESULT 10
 ADQ90729
 ID ADQ90729 standard; protein; 479 AA.

AC ADQ90729;

XX 21-OCT-2004 (first entry)

XX Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:5.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.

XX Homo sapiens.
 OS Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90700.

XX Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

XX Example 2; SEQ ID NO 5; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain,
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup

CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 XX

SQ Sequence 479 AA;

Query Match 100.0%; Score 58; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTFTNYGIN 10
 |||||
 Db 49 GYFTFTNYGIN 58

RESULT 11

ADQ90731

ID ADQ90731 standard; protein; 479 AA.

XX AC ADQ90731;

XX 21-OCT-2004 (first entry)

XX Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:9.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.

XX Homo sapiens.
 OS Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90704.

XX Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

XX Example 2; SEQ ID NO 9; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding

CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

XX Sequence 479 AA;

Query Match 100.0%; Score 58; DB 8; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFNTNYGIN 10
 |||||
 Db 49 GYTFNTNYGIN 58

RESULT 12

ID ABR83196 standard; protein; 120 AA.

AC ABR83196;

DT 15-JAN-2004 (first entry)

XX Chimeric LL1 antibody heavy chain variable region (cLL1VH).

DE LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
 KW immunomodulator; cLL1; chimeric.

XX Chimeric - Mus sp.

OS WO2003074567-A2.

PN 12-SEP-2003.

XX 03-MAR-2003; 2003WO-GB000890.

PF 01-MAR-2002; 2002US-0360259P.

XX (IMMU-) IMMUNOMEDICS INC.

PA (MCCA/) MCCA J D.

XX Hansen H, Leung S, Qu Z, Goldenberg DM;

XX WPI; 2003-767381/72.

DR N-PSDB; ACF57896.

XX New humanized, human or chimeric anti-CD74 antibody or fragment, useful
 PT for diagnosing or treating a CD74 expressing malignancy, an immune
 PT dysregulation disease, an autoimmune disease or graft versus host
 PT disease.

XX Claim 13; Fig 2A; 91pp; English.

XX

CC The invention relates to a humanized, human or chimeric anti-CD74
 CC antibody or its fragment. The naked anti-CD74 antibody or a naked
 CC antibody fusion protein or fragment, or a therapeutic or diagnostic
 CC conjugate comprising an anti-CD74 antibody is useful for diagnosing or
 CC treating a disorder or a disease that is a CD74 expressing malignancy
 CC (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
 CC myeloma, another B-cell malignancy and a T-cell malignancy), an immune
 CC dysregulation disease, an autoimmune disease, organ graft rejection, and
 CC graft versus host disease. The solid tumour is melanoma, carcinoma and
 CC sarcoma. The carcinoma is a renal carcinoma, lung carcinoma, intestinal
 CC carcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of
 CC non-Hodgkin's lymphoma, Hodgkin's lymphoma, indolent forms of B-cell
 CC lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic
 CC leukemias, acute lymphatic leukemias, and multiple myeloma. The present
 CC sequence represents a chimeric anti-CD74 antibody LL1 (cLL1) heavy chain
 CC variable region

XX Sequence 120 AA;

Query Match 98.3%; Score 57; DB 7; Length 120;
 Best Local Similarity 90.0%; Pred. No. 0.21;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFNTNYGIN 10
 |||||
 Db 26 GYTFNTNYGVN 35

RESULT 13

ABR83194

ID ABR83194 standard; protein; 120 AA.

AC ABR83194;

DT 15-JAN-2004 (first entry)

XX Murine LL1 antibody heavy chain variable region (LL1VH).

DE LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
 KW immunomodulator; mLL1.

XX Mus sp.

XX WO2003074567-A2.

XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-GB000890.

XX 01-MAR-2002; 2002US-0360259P.

XX (IMMU-) IMMUNOMEDICS INC.

PA (MCCA/) MCCA J D.

XX Hansen H, Leung S, Qu Z, Goldenberg DM;

XX WPI; 2003-767381/72.

DR N-PSDB; ACF57894.

XX New humanized, human or chimeric anti-CD74 antibody or fragment, useful
 PT for diagnosing or treating a CD74 expressing malignancy, an immune
 PT dysregulation disease, an autoimmune disease or graft versus host
 PT disease.

XX Claim 6; Fig 3A; 91pp; English.

XX The invention relates to a humanized, human or chimeric anti-CD74
 CC antibody or its fragment. The naked anti-CD74 antibody or a naked
 CC antibody fusion protein or fragment, or a therapeutic or diagnostic
 CC conjugate comprising an anti-CD74 antibody is useful for diagnosing or
 CC treating a disorder or a disease that is a CD74 expressing malignancy
 CC (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
 CC myeloma, another B-cell malignancy and a T-cell malignancy), an immune

CC dysregulation disease, an autoimmune disease, organ graft rejection, and
 CC graft versus host disease. The solid tumour is melanoma, carcinoma and
 CC sarcoma. The carcinoma is a renal carcinoma, lung carcinoma, intestinal
 CC carcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of
 CC non-Hodgkin's lymphoma, Hodgkin's lymphoma, indolent forms of B-cell
 CC lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic
 CC leukemias, acute lymphatic leukemias, and multiple myeloma. The present
 CC sequence represents a murine anti-CD74 antibody LL1 heavy chain variable
 CC region

XX SQ Sequence 120 AA;

Query Match 98.3%; Score 57; DB 7; Length 120;
 Best Local Similarity 90.0%; Pred. No. 0.21;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
 |||||:|
 Db 26 GYFTNYGVN 35

RESULT 14

ABR83198
 ID ABR83198 standard; protein; 120 AA.
 XX
 AC ABR83198;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Humanised LL1 antibody heavy chain variable region (hLL1VH).
 XX
 KW LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
 KW immunomodulator; hLL1.
 XX
 OS Homo sapiens.
 XX
 PN WO2003074567-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 03-MAR-2003; 2003WO-GB000890.
 XX
 PR 01-MAR-2002; 2002US-0360259P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 PA (MCCA/) MCCALL J D.
 XX
 PI Hansen H, Leung S, Qu Z, Goldenberg DM;
 XX
 DR WPI; 2003-767381/72.
 DR N-PSDB; ACF57898.
 XX
 PF New humanized, human or chimeric anti-CD74 antibody or fragment, useful
 PT for diagnosing or treating a CD74 expressing malignancy, an immune
 PT dysregulation disease, an autoimmune disease or graft versus host
 PT disease.

XX PS Claim 7; Fig 4A; 91pp; English.

XX
 CC The invention relates to a humanised, human or chimeric anti-CD74
 CC antibody or its fragment. The naked anti-CD74 antibody or a naked
 CC antibody fusion protein or fragment, or a therapeutic or diagnostic
 CC conjugate comprising an anti-CD74 antibody is useful for diagnosing or
 CC treating a disorder or a disease that is a CD74 expressing malignancy
 CC (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
 CC myeloma, another B-cell malignancy and a T-cell malignancy), an immune
 CC dysregulation disease, an autoimmune disease, organ graft rejection, and
 CC graft versus host disease. The solid tumour is melanoma, carcinoma and
 CC sarcoma. The carcinoma is a renal carcinoma, lung carcinoma, intestinal
 CC carcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of
 CC non-Hodgkin's lymphoma, Hodgkin's lymphoma, indolent forms of B-cell
 CC lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic
 CC leukemias, acute lymphatic leukemias, and multiple myeloma. The present

CC sequence represents a humanised anti-CD74 antibody LL1 (hLL1) heavy chain
 CC variable region

XX SQ Sequence 120 AA;

Query Match 98.3%; Score 57; DB 7; Length 120;
 Best Local Similarity 90.0%; Pred. No. 0.21;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
 |||||:|
 Db 26 GYFTNYGVN 35

RESULT 15

ADU26544
 ID ADU26544 standard; protein; 120 AA.
 XX
 AC ADU26544;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Chimeric LL1 antibody heavy chain variable region segid 6.
 XX
 KW immunosuppressive; cytostatic; immunomodulatory; immunotoxin;
 KW radioimmunotherapeutic; immunoconjugate; anti-CD74 antibody;
 KW CD74-expressing malignancy; immune dysregulation disease;
 KW autoimmune disease; organ-graft rejection; graft-versus-host disease;
 KW solid tumor; non-Hodgkin's lymphoma; Hodgkin's lymphoma;
 KW multiple myeloma; B-cell malignancy; T-cell malignancy; melanoma;
 KW carcinoma; sarcoma; glioma; mouse; LL1; heavy chain variable region;
 KW human.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT Region 50..66
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT Region 99..109
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 XX
 PN US2004219203-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 12-NOV-2003; 2003US-00706852.
 XX
 PR 10-MAY-1999; 99US-00307816.
 PR 09-JUN-2000; 2000US-00590284.
 PR 01-OCT-2001; 2001US-00965796.
 PR 01-MAR-2002; 2002US-0360259P.
 PR 09-DEC-2002; 2002US-00314330.
 PR 24-JAN-2003; 2003US-00350096.
 PR 03-MAR-2003; 2003US-00377122.
 PR 17-JUN-2003; 2003US-0478830P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Griffiths GL, Hansen HJ, Goldenberg DM, Lundberg BB;
 XX
 DR WPI; 2005-010089/01.
 DR N-PSDB; ADU26543.
 XX
 PF Composition useful in treating and/or diagnosing, for example, graft-
 PT versus-host disease or CD74-expressing malignancy, comprises
 PT immunoconjugate having anti-CD74 binding molecules conjugated to lipids,

PT polymeric carriers, and effectors.
XX
XX Disclosure; SEQ ID NO 6; 44pp; English.
XX
CC The invention describes a composition (I) comprising an immunoconjugate
CC which has one or more anti-CD74 binding molecules conjugated to one or
CC more lipids, polymeric carriers, micelles, nanoparticles or their
CC combinations, and one or more effectors. Also described are: preparing
CC (MI) a carrier, involving mixing one or more amphiphilic lipids with an
CC effector to form a carrier, and contacting the carrier with an anti-CD74
CC antibody; and a kit comprising (I). (I) is useful for treating and/or
CC diagnosing a disease or disorder such as a CD74-expressing malignancy,
CC immune dysregulation disease, autoimmune disease, organ-graft rejection
CC and graft-versus-host disease. The CD74-expressing malignancy is chosen
CC from solid tumor, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
CC myeloma, B-cell malignancy, and T-cell malignancy. The disease or
CC disorder is CD74-expressing malignancy other than lymphoma or leukemia.
CC The CD74-expressing malignancy is a solid tumor, which is chosen from
CC melanoma, carcinoma, sarcoma and glioma. The carcinoma is chosen from
CC renal carcinoma, lung carcinoma, intestinal carcinoma, stomach carcinoma,
CC breast carcinoma, prostate cancer, ovarian cancer, and melanoma. The CD74
CC -expressing malignancy is a B-cell malignancy chosen from indolent forms
CC of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic
CC lymphatic leukemias, acute lymphatic leukemias and multiple myeloma. (I)
CC comprises LL1 or its fragment. The composition further comprises one or
CC more additional antibodies or their fragments chosen from anti-CD19, anti
CC -CD20, anti-CD22, anti-CD30, anti-CD33, anti-TAC and their mixtures. The effector
CC antigen (HLA)-DR, anti-MUC1, anti-TAC and their mixtures. The effector
CC molecule comprises one or more drugs, prodrugs, toxins, enzymes,
CC radioisotopes, immunomodulators, cytokines, hormones, antibodies,
CC oligonucleotides or their combinations. The diagnostic agent comprises
CC one or more image enhancing agents and the method further involves
CC performing magnetic resonance imaging (MRI). The composition comprises
CC one or more ultrasound contrast agents, where the ultrasound contrast
CC agent includes a liposome or dextran. The immunoconjugate of (I) has a
CC significant effect in evocation of a humoral and/or cellular immune
CC response in a mammal. This is the amino acid sequence of a chimeric LL1
CC (or anti-CD74 antibody) heavy chain variable regions suitable for use in
XX the immunoconjugate of the invention.
SQ Sequence 120 AA;

Query Match 98.3%; Score 57; DB 9; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGIN 10
|||
Db 26 GYFTNYGVN 35

Search completed: April 25, 2006, 06:15:04
Job time : 55.3962 secs

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